(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
12 May 2005 (12.05.2005)

PCT

(10) International Publication Number
WO 2005/043162 A2

(51) International Patent Classification[7]: G01N 33/574, C12Q 1/68

(21) International Application Number: PCT/EP2004/012464

(22) International Filing Date: 4 November 2004 (04.11.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
03025339.7 4 November 2003 (04.11.2003) EP

(71) Applicant *(for DE only)*: **ROCHE DIAGNOSTICS GMBH** [DE/DE]; Sandhofer Str. 116, 68305 Mannheim (DE).

(71) Applicant *(for all designated States except DE, US)*: **F.HOFFMANN-LA ROCHE AG** [CH/CH]; Grenzacherstrasse 124, CH-4070 Basel (CH).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **HAFERLACH, Torsten** [DE/DE]; Springerstrasse 8, 81477 München (DE). **DUGAS, Martin** [DE/DE]; Michael-Fischer-Platz 6, 94469 Deggendorf (DE). **KERN, Wolfgang** [DE/DE]; Hanfelder Strasse 101, 82319 Starnberg (DE). **KOHLMANN, Alexander** [DE/DE]; Schwarzstrasse 14, 92318 Neumarkt (DE). **MERGENTHALER, Susanne** [DE/CH]; Muehlhauserstrasse 69, CH-4056 Basel (CH). **SCHNITTGER, Susanne** [DE/DE]; Saalburgstrasse 2a, 81375 München (DE). **SCHOCH, Claudia** [DE/DE]; Springerstrasse 8, 81477 München (DE).

(74) Common Representative: **ROCHE DIAGNOSTICS GMBH**; C/O Burger Alexander, Patent Department (TR-E), Postfach 11 52, 82372 Penzberg (DE).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHOD FOR DISTINGUISHING MLL-PTD-POSITIVE AML FROM OTHER AML SUBTYPES

(57) Abstract: Disclosed is a method for distinguishing MLL-PTD-positive AML from other AML subtypes in a sample by determining the expression level of markers, as well as a diagnostic kit and an apparatus containing the markers.

WO 2005/043162 A2

Method for distinguishing MLL-PTD-positive AML from other AML subtypes

The present invention is directed to a method for distinguishing MLL-PTD-positive AML from other AML subtypes by determining the expression level of selected marker genes.

Leukemias are classified into four different groups or types: acute myeloid (AML), acute lymphatic (ALL), chronic myeloid (CML) and chronic lymphatic leukemia (CLL). Within these groups, several subcategories can be identified further using a panel of standard techniques as described below. These different subcategories in leukemias are associated with varying clinical outcome and therefore are the basis for different treatment strategies. The importance of highly specific classification may be illustrated in detail further for the AML as a very heterogeneous group of diseases. Effort is aimed at identifying biological entities and to distinguish and classify subgroups of AML which are associated with a favorable, intermediate or unfavorable prognosis, respectively. In 1976, the FAB classification was proposed by the French-American-British co-operative group which was based on cytomorphology and cytochemistry in order to separate AML subgroups according to the morphological appearance of blasts in the blood and bone marrow. In addition, it was recognized that genetic abnormalities occurring in the leukemic blast had a major impact on the morphological picture and even more on the prognosis. So far, the karyotype of the leukemic blasts is the most important independent prognostic factor regarding response to therapy as well as survival.

Usually, a combination of methods is necessary to obtain the most important information in leukemia diagnostics: Analysis of the morphology and cytochemistry of bone marrow blasts and peripheral blood cells is necessary to establish the diagnosis. In some cases the addition of immunophenotyping is mandatory to separate very undifferentiated AML from acute lymphoblastic leukemia and CLL. Leukemia subtypes investigated can be diagnosed by cytomorphology alone, only if an expert reviews the smears. However, a genetic analysis based on chromosome analysis, fluorescence in situ hybridization or RT-PCR and immunophenotyping is required in order to assign all cases in to the right category. The aim of these techniques besides diagnosis is mainly to determine the

prognosis of the leukemia. A major disadvantage of these methods, however, is that viable cells are necessary as the cells for genetic analysis have to divide in vitro in order to obtain metaphases for the analysis. Another problem is the long time of 72 hours from receipt of the material in the laboratory to obtain the result. Furthermore, great experience in preparation of chromosomes and even more in analyzing the karyotypes is required to obtain the correct result in at least 90% of cases. Using these techniques in combination, hematological malignancies in a first approach are separated into chronic myeloid leukemia (CML), chronic lymphatic (CLL), acute lymphoblastic (ALL), and acute myeloid leukemia (AML). Within the latter three disease entities several prognostically relevant subtypes have been established. As a second approach this further sub-classification is based mainly on genetic abnormalities of the leukemic blasts and clearly is associated with different prognoses.

The sub-classification of leukemias becomes increasingly important to guide therapy. The development of new, specific drugs and treatment approaches requires the identification of specific subtypes that may benefit from a distinct therapeutic protocol and, thus, can improve outcome of distinct subsets of leukemia. For example, the new therapeutic drug (STI571, Imatinib) inhibits the CML specific chimeric tyrosine kinase BCR-ABL generated from the genetic defect observed in CML, the BCR-ABL-rearrangement due to the translocation between chromosomes 9 and 22 (t(9;22) (q34; q11)). In patients treated with this new drug, the therapy response is dramatically higher as compared to all other drugs that had been used so far. Another example is the subtype of acute myeloid leukemia AML M3 and its variant M3v both with karyotype t(15;17)(q22; q11-12). The introduction of a new drug (all-trans retinoic acid - ATRA) has improved the outcome in this subgroup of patient from about 50% to 85 % long-term survivors. As it is mandatory for these patients suffering from these specific leukemia subtypes to be identified as fast as possible so that the best therapy can be applied, diagnostics today must accomplish sub-classification with maximal precision. Not only for these subtypes but also for several other leukemia subtypes different treatment approaches could improve outcome. Therefore, rapid and precise identification of distinct leukemia subtypes is the future goal for diagnostics.

Thus, the technical problem underlying the present invention was to provide means for leukemia diagnostics which overcome at least some of the disadvantages of the prior art diagnostic methods, in particular encompassing the time-consuming and unreliable combination of different methods and which provides a rapid assay to unambiguously distinguish one AML subtype from another, e.g. by genetic analysis.

According to Golub et al. (Science, 1999, 286, 531-7), gene expression profiles can be used for class prediction and discriminating AML from ALL samples. However, for the analysis of acute leukemias the selection of the two different subgroups was performed using exclusively morphologic-phenotypical criteria. This was only descriptive and does not provide deeper insights into the pathogenesis or the underlying biology of the leukemia. The approach reproduces only very basic knowledge of cytomorphology and intends to differentiate classes. The data is not sufficient to predict prognostically relevant cytogenetic aberrations.

Furthermore, the international application WO-A 03/039443 discloses marker genes the expression levels of which are characteristic for certain leukemia, e.g. AML subtypes and additionally discloses methods for differentiating between the subtype of AML cells by determining the expression profile of the disclosed marker genes. However, WO-A 03/039443 does not provide guidance which set of distinct genes discriminate between two subtypes and, as such, can be routineously taken in order to distinguish one AML subtype from another.

The problem is solved by the present invention, which provides a method for distinguishing MLL-PTD-positive AML from other AML subtypes in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, and/or 3,

wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1

is indicative for the presence of PTD (MLL-PTD-positive AML with normal karyotype) when PTD is distinguished from AML_NK (MLL-PTD-negative AML with normal karyotype),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 12, 14, 15, 16, 18, 19, 20, 21, 22, 23, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 44, 45, 47, 48, 49, and/or 50 of Table 2.1, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 10, 13, 17, 24, 25, 41, 43, and/or 46, of Table 2.1,

is indicative for M4eo when M4eo is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 26, 28, 29, 31, 32, 33, 34, 35, 36, 38, 39, 41, 42, 44, 45, 46, 48, 49, and/or 50 of Table 2.2, and/or

a higher expression of 5, 13, 18, 27, 30, 37, 40, 43, and/or 47, of Table 2.2

is indicative for PTD when PTD is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 49, and/or 50 of Table 2.3, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 34, and/or 48, of Table 2.3

is indicative for inv3 when inv3 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 5, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 23, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 41, 42, 43, 44, 45, 46, 47, 48, and/or 50 of Table 2.4, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 4, 6, 7, 8, 22, 24, 40, and/or 49, of Table 2.4

is indicative for t(15;17) when t(15;17) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 2.5

is indicative for t(8;21) when t(8;21) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 43, 45, 46, 47, 48, 49, and/or 50 of Table 2.6, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 12, 15, 29, 41, and/or 44, of Table 2.6

is indicative for tMLL when tMLL is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 4, 5, 7, 10, 12, 13, 16, 17, 19, 23, 25, 30, 31, 32, 33, 34, 37, 41, 43, 45, 47, 48, and/or 50 of Table 3.1,and/or

a higher expression a polynucleotide defined by any of the numbers 3, 6, 8, 9, 11, 14, 15, 18, 20, 21, 22, 24, 26, 27, 28, 29, 35, 36, 38, 39, 40, 42, 44, 46, and/or 49, of Table 3.1,

is indicative for M4eo when M4eo is distinguished from PTD,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 5, 6, 9, 12, 23, 28, 38, 41, 44, 45, 46, and/or 47, of Table 3.2, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 7, 8, 10, 11, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 24, 25, 26, 27, 29, 30, 31, 32, 33, 34, 35, 36, 37, 39, 40, 42, 43, 48, 49, and/or 50 of Table 3.2,

is indicative for M4eo when M4eo is distinguished from inv3,

a lower expression of at least one polynucleotide defined by any of the numbers 2, 3, 4, 6, 11, 14, 20, 22, 26, 31, 32, 33, 34, 39, 40, 41, and/or 48, of Table 3.3, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 5, 7, 8, 9, 10, 12, 13, 15, 16, 17, 18, 19, 21, 23, 24, 25, 27, 28, 29, 30, 35, 36, 37, 38, 42, 43, 44, 45, 46, 47, 49, and/or 50 of Table 3.3,

is indicative for M4eo when M4eo is distinguished from t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 7, 31, 40, and/or 49, of Table 3.4, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 32, 33, 34, 35, 36, 37, 38, 39, 41, 42, 43, 44, 45, 46, 47, 48, and/or 50 of Table 3.4

is indicative for M4eo when M4eo is distinguished from t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 3, 10, 14, 17, 18, 19, 21, 24, 25, 26, 31, 32, 34, 41, 44, and/or 50 of Table 3.5, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 2, 4, 5, 6, 7, 8, 9, 11, 12, 13, 15, 16, 20, 22, 23, 27, 28, 29, 30, 33, 35, 36, 37, 38, 39, 40, 42, 43, 45, 46, 47, 48, and/or 49, of Table 3.5

is indicative for M4eo when M4eo is distinguished from tMLL,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 4, 6, 9, 28, 30, 32, 35, 37, 44, 45, and/or 48, of Table 3.6, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 5, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 29, 31, 33, 34, 36, 38, 39, 40, 41, 42, 43, 46, 47, 49, and/or 50 of Table 3.6

is indicative for PTD when PTD is distinguished from inv3,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 6, 7, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 23, 27, 28, 29, 30, 31, 32, 33, 34, 36, 38, 39, 41, 43, 44, 45, 47, 48, and/or 50 of Table 3.7, and/or

a higher expression of polynucleotide defined by any of the numbers 5, 8, 9, 19, 21, 22, 24, 25, 26, 35, 37, 40, 42, 46, and/or 49, of Table 3.7,

is for PTD when PTD is distinguished from t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 7, 9, 10, 11, 13, 16, 20, 21, 22, 23, 30, 35, 36, 38, 42, 45, and/or 50 of Table 3.8, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 8, 12, 14, 15, 17, 18, 19, 24, 25, 26, 27, 28, 29, 31, 32, 33, 34, 37, 39, 40, 41, 43, 44, 46, 47, 48, and/or 49, of Table 3.8

is indicative for PTD when PTD is distinguished from t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 5, 8, 10, 11, 13, 15, 17, 19, 25, 26, 28, 29, 34, and/or 46, of Table 3.9, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 2, 3, 4, 6, 7, 9, 12, 14, 16, 18, 20, 21, 22, 23, 24, 27, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 47, 48, 49, and/or 50 of Table 3.9

is indicative for PTD when PTD is distinguished from tMLL,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 23, 24, 25, 26, 28, 29, 32, 33, 36, 38, 39, 40, 43, 44, 45, 46, 47, and/or 49, of Table 3.10, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 22, 27, 30, 31, 34, 35, 37, 41, 42, 48, and/or 50 of Table 3.10,

is indicative for inv(3) when inv(3) is distinguished from t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 5, 6, 9, 11, 12, 15, 17, 18, 19, 23, 27, 35, 36, 37, 39, 42, 43, 47, 49, and/or 50 of Table 3.11, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 2, 3, 4, 7, 8, 10, 13, 14, 16, 20, 21, 22, 24, 25, 26, 28, 29, 30, 31, 32, 33, 34, 38, 40, 41, 44, 45, 46, and/or 48, of Table 3.11

is indicative for inv(3) when inv(3) is distinguished from t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 3, 4, 6, 7, 8, 12, 14, 15, 16, 17, 18, 19, 20, 21, 23, 25, 26, 28, 29, 30, 31, 33, 34, 35, 37, 38, 39, 42, 43, 44, 45, 47, 48, and/or 50 of Table 3.12, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 2, 5, 9, 10, 11, 13, 22, 24, 27, 32, 36, 40, 41, 46, and/or 49, of Table 3.12

is indicative for inv(3) when inv(3) is distinguished from tMLL,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 3, 4, 7, 14, 16, 20, 22, 23, 24, 25, 26, 30, 35, 36, 37, 39, 40, 43, 44, 46, and/or 50 of Table 3.13, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 5, 6, 8, 9, 10, 11, 12, 13, 15, 17, 18, 19, 21, 27, 28, 29, 31, 32, 33, 34, 38, 41, 42, 45, 47, 48, and/or 49 of Table 3.13,

is indicative for t(15;17) when t(15;17) is distinguished from t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 13, 15, 25, 26, 27, 28, 30, 32, 33, 35, 36, 38, 39, 43, 48, and/or 49, of Table 3.14, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 29, 31, 34, 37, 40, 41, 42, 44, 45, 46, 47, and/or 50 of Table 3.14,

is indicative for t(15;17) when t(15;17) is distinguished from tMLL,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 15, 16, 18, 19, 21, 23, 24, 25, 26, 27, 28, 29, 30, 32, 33, 34, 35, 36, 38, 39, 40, 41, 42, 43, 44, 47, 48, of Table 3.15, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 12, 14, 17, 20, 22, 31, 37, 45, 46, 49, and/or 50 of Table 3.15,

is indicative for t(8;21) when t(8;21) is distinguished from tMLL.

As used herein, the following definitions apply to the above used abbreviations (see also example 1):

tMLL: AML with translocations in the MLL gene (t(11q23)/MLL)

PTD: AML with normal karyotype and Partial Tandem Duplication (PTD) within the MLL gene (MLL-PTD)

AML_NK	AML with normal karyotype (no Partial Tandem Duplication (PTD) within the MLL gene)
t(8;21)	AML with translocation t(8;21)
t(15;17)	AML with translocation t(15;17)
t(inv3)	AML with inversion 3
M4eo	AML with inversion 16 (inv(16))

As used herein, "all other subtypes" refer to the subtypes of the present invention, i.e. if one subtype is distinguished from "all other subtypes", it is distiguished from all other subtypes contained in the present invention.

According to the present invention, a "sample" means any biological material containing genetic information in the form of nucleic acids or proteins obtainable or obtained from an individual. The sample includes e.g. tissue samples, cell samples, bone marrow and/or body fluids such as blood, saliva, semen. Preferably, the sample is blood or bone marrow, more preferably the sample is bone marrow. The person skilled in the art is aware of methods, how to isolate nucleic acids and proteins from a sample. A general method for isolating and preparing nucleic acids from a sample is outlined in Example 3.

According to the present invention, the term "lower expression" is generally assigned to all by numbers and Affymetrix Id. definable polynucleotides the t-values and fold change (fc) values of which are negative, as indicated in the Tables. Accordingly, the term "higher expression" is generally assigned to all by numbers and Affymetrix Id. definable polynucleotides the t-values and fold change (fc) values of which are positive.

According to the present invention, the term "expression" refers to the process by which mRNA or a polypeptide is produced based on the nucleic acid sequence of a gene, i.e. „expression" also includes the formation of mRNA upon transcription. In accordance with the present invention, the term „determining the expression level"

preferably refers to the determination of the level of expression, namely of the markers.

Generally, "marker" refers to any genetically controlled difference which can be used in the genetic analysis of a test versus a control sample, for the purpose of assigning the sample to a defined genotype or phenotype. As used herein, "markers" refer to genes which are differentially expressed in, e.g., different AML subtypes. The markers can be defined by their gene symbol name, their encoded protein name, their transcript identification number (cluster identification number), the data base accession number, public accession number or GenBank identifier or, as done in the present invention, Affymetrix identification number, chromosomal location, UniGene accession number and cluster type, LocusLink accession number (see Examples and Tables).

The Affymetrix identification number (affy id) is accessible for anyone and the person skilled in the art by entering the "gene expression omnibus" internet page of the National Center for Biotechnology Information (NCBI) (http://www.ncbi.nlm.nih.gov/geo/). In particular, the affy id's of the polynucleotides used for the method of the present invention are derived from the so-called U133 chip. The sequence data of each identification number can be viewed at http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL96

Generally, the expression level of a marker is determined by the determining the expression of its corresponding "polynucleotide" as described hereinafter.

According to the present invention, the term „polynucleotide" refers, generally, to a DNA, in particular cDNA, or RNA, in particular a cRNA, or a portion thereof or a polypeptide or a portion thereof. In the case of RNA (or cDNA), the polynucleotide is formed upon transcription of a nucleotide sequence which is capable of expression. The polynucleotide fragments refer to fragments preferably of between at least 8, such as 10, 12, 15 or 18 nucleotides and at least 50, such as 60, 80, 100, 200 or 300 nucleotides in length, or a complementary sequence thereto, representing a consecutive stretch of nucleotides of a gene, cDNA or mRNA. In other terms, polynucleotides include also any fragment (or complementary

sequence thereto) of a sequence derived from any of the markers defined above as long as these fragments unambiguously identify the marker.

The determination of the expression level may be effected at the transcriptional or translational level, i.e. at the level of mRNA or at the protein level. Protein fragments such as peptides or polypeptides advantageously comprise between at least 6 and at least 25, such as 30, 40, 80, 100 or 200 consecutive amino acids representative of the corresponding full length protein. Six amino acids are generally recognized as the lowest peptidic stretch giving rise to a linear epitope recognized by an antibody, fragment or derivative thereof. Alternatively, the proteins or fragments thereof may be analysed using nucleic acid molecules specifically binding to three-dimensional structures (aptamers).

Depending on the nature of the polynucleotide or polypeptide, the determination of the expression levels may be effected by a variety of methods. For determining and detecting the expression level, it is preferred in the present invention that the polynucleotide, in particular the cRNA, is labelled.

The labelling of the polynucleotide or a polypeptide can occur by a variety of methods known to the skilled artisan. The label can be fluorescent, chemiluminescent, bioluminescent, radioactive (such as ^{3}H or ^{32}P). The labelling compound can be any labelling compound being suitable for the labelling of polynucleotides and/or polypeptides. Examples include fluorescent dyes, such as fluorescein, dichlorofluorescein, hexachlorofluorescein, BODIPY variants, ROX, tetramethylrhodamin, rhodamin X, Cyanine-2, Cyanine-3, Cyanine-5, Cyanine-7, IRD40, FluorX, Oregon Green, Alexa variants (available e.g. from Molecular Probes or Amersham Biosciences) and the like, biotin or biotinylated nucleotides, digoxigenin, radioisotopes, antibodies, enzymes and receptors. Depending on the type of labelling, the detection is done via fluorescence measurements, conjugation to streptavidin and/or avidin, antigen-antibody- and/or antibody-antibody-interactions, radioactivity measurements, as well as catalytic and/or receptor/ligand interactions. Suitable methods include the direct labelling (incorporation) method, the amino-modified (amino-allyl) nucleotide method (available e.g. from Ambion), and the primer tagging method (DNA dendrimer labelling, as kit available e.g. from Genisphere). Particularly preferred for the present invention is the use of

biotin or biotinylated nucleotides for labelling, with the latter being directly incorporated into, e.g. the cRNA polynucleotide by in vitro transcription.

If the polynucleotide is mRNA, cDNA may be prepared into which a detectable label, as exemplified above, is incorporated. Said detectably labelled cDNA, in single-stranded form, may then be hybridised, preferably under stringent or highly stringent conditions to a panel of single-stranded oligonucleotides representing different genes and affixed to a solid support such as a chip. Upon applying appropriate washing steps, those cDNAs will be detected or quantitatively detected that have a counterpart in the oligonucleotide panel. Various advantageous embodiments of this general method are feasible. For example, the mRNA or the cDNA may be amplified e.g. by polymerase chain reaction, wherein it is preferable, for quantitative assessments, that the number of amplified copies corresponds relative to further amplified mRNAs or cDNAs to the number of mRNAs originally present in the cell. In a preferred embodiment of the present in ivention, the cDNAs are transcribed into cRNAs prior to the hybridisation step wherein only in the transcription step a label is incorporated into the nucleic acid and wherein the cRNA is employed for hybridisation. Alternatively, the label may be attached subsequent to the transcription step.

Similarly, proteins from a cell or tissue under investigation may be contacted with a panel of aptamers or of antibodies or fragments or derivatives thereof. The antibodies etc. may be affixed to a solid support such as a chip. Binding of proteins indicative of an AML subtype may be verified by binding to a detectably labelled secondary antibody or aptamer. For the labelling of antibodies, it is referred to Harlow and Lane, "Antibodies, a laboratory manual", CSH Press, 1988, Cold Spring Harbor. Specifically, a minimum set of proteins necessary for diagnosis of all AML subtypes may be selected for creation of a protein array system to make diagnosis on a protein lysate of a diagnostic bone marrow sample directly. Protein Array Systems for the detection of specific protein expression profiles already are available (for example: Bio-Plex, BIORAD, München, Germany). For this application preferably antibodies against the proteins have to be produced and immobilized on a platform e.g. glasslides or microtiterplates. The immobilized antibodies can be labelled with a reactant specific for the certain target proteins as

discussed above. The reactants can include enzyme substrates, DNA, receptors, antigens or antibodies to create for example a capture sandwich immunoassay.

For reliably distinguishing MLL-PTD-positive AML from other AML subtypes in a sample it is useful that the expression of more than one of the above defined markers is determined. As a criterion for the choice of markers, the statistical significance of markers as expressed in q or p values based on the concept of the false discovery rate is determined. In doing so, a measure of statistical significance called the *q* value is associated with each tested feature. The *q* value is similar to the *p* value, except it is a measure of significance in terms of the false discovery rate rather than the false positive rate (Storey JD and Tibshirani R. Proc.Natl.Acad.Sci., 2003, Vol. 100:9440-5.

In a preferred embodiment of the present invention, markers as defined in Table 1.1-3.15 having a q-value of less than 3E-03, more preferred less than 1.5E-09, most preferred less than 1.5E-11, less than 1.5E-20, less than 1.5E-30, are measured.

Of the above defined markers, the expression level of at least two, preferably of at least ten, more preferably of at least 25, most preferably of 50 of at least one of the Tables of the markers is determined.

In another preferred embodiment, the expression level of at least 2, of at least 5, of at least 10 out of the markers having the numbers 1 – 10, 1-20, 1-40, 1-50 of at least one of the Tables are measured.

The level of the expression of the „marker", i.e. the expression of the polynucleotide is indicative of the AML subtype of a cell or an organism. The level of expression of a marker or group of markers is measured and is compared with the level of expression of the same marker or the same group of markers from other cells or samples. The comparison may be effected in an actual experiment or in silico. When the expression level also referred to as expression pattern or expression signature (expression profile) is measurably different, there is according to the invention a meaningful difference in the level of expression. Preferably the difference at least is 5 %, 10% or 20%, more preferred at least 50% or may even be as high as 75% or 100%. More preferred the difference in the level of expression is

at least 200%, i.e. two fold, at least 500%, i.e. five fold, or at least 1000%, i.e. 10 fold.

Accordingly, the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold lower, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold lower in the first subtype. On the other hand, the expression level of markers expressed higher in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold higher, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold higher in the first subtype.

In another embodiment of the present invention, the sample is derived from an individual having leukaemia, preferably AML.

For the method of the present invention it is preferred if the polynucleotide the expression level of which is determined is in form of a transcribed polynucleotide. A particularly preferred transcribed polynucleotide is an mRNA, a cDNA and/or a cRNA, with the latter being preferred. Transcribed polynucleotides are isolated from a sample, reverse transcribed and/or amplified, and labelled, by employing methods well-known the person skilled in the art (see Example 3). In a preferred embodiment of the methods according to the invention, the step of determining the expression profile further comprises amplifying the transcribed polynucleotide.

In order to determine the expression level of the transcribed polynucleotide by the method of the present invention, it is preferred that the method comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions, as described hereinafter.

The term "hybridizing" means hybridization under conventional hybridization conditions, preferably under stringent conditions as described, for example, in Sambrook, J., et al., in "Molecular Cloning: A Laboratory Manual" (1989), Eds. J. Sambrook, E. F. Fritsch and T. Maniatis, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, NY and the further definitions provided above. Such

conditions are, for example, hybridization in 6x SSC, pH 7.0 / 0.1% SDS at about 45°C for 18-23 hours, followed by a washing step with 2x SSC/0.1% SDS at 50°C. In order to select the stringency, the salt concentration in the washing step can for example be chosen between 2x SSC/0.1% SDS at room temperature for low stringency and 0.2x SSC/0.1% SDS at 50°C for high stringency. In addition, the temperature of the washing step can be varied between room temperature, ca. 22°C, for low stringency, and 65°C to 70° C for high stringency. Also contemplated are polynucleotides that hybridize at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation, preferably of formamide concentration (lower percentages of formamide result in lowered stringency), salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH2PO4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 mg/ml salmon sperm blocking DNA, followed by washes at 50°C with 1 X SSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5x SSC). Variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

"Complementary" and "complementarity", respectively, can be described by the percentage, i.e. proportion, of nucleotides which can form base pairs between two polynucleotide strands or within a specific region or domain of the two strands. Generally, complementary nucleotides are, according to the base pairing rules, adenine and thymine (or adenine and uracil), and cytosine and guanine. Complementarity may be partial, in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be a complete or total complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has effects on the efficiency and strength of hybridization between nucleic acid strands.

Two nucleic acid strands are considered to be 100% complementary to each other over a defined length if in a defined region all adenines of a first strand can pair

with a thymine (or an uracil) of a second strand, all guanines of a first strand can pair with a cytosine of a second strand, all thymine (or uracils) of a first strand can pair with an adenine of a second strand, and all cytosines of a first strand can pair with a guanine of a second strand, and vice versa. According to the present invention, the degree of complementarity is determined over a stretch of 20, preferably 25, nucleotides, i.e. a 60% complementarity means that within a region of 20 nucleotides of two nucleic acid strands 12 nucleotides of the first strand can base pair with 12 nucleotides of the second strand according to the above ruling, either as a stretch of 12 contiguous nucleotides or interspersed by non-pairing nucleotides, when the two strands are attached to each other over said region of 20 nucleotides. The degree of complementarity can range from at least about 50% to full, i.e. 100% complementarity. Two single nucleic acid strands are said to be "substantially complementary" when they are at least about 80% complementary, preferably about 90% or higher. For carrying out the method of the present invention substantial complementarity is preferred.

Preferred methods for detection and quantification of the amount of polynucleotides, i.e. for the methods according to the invention allowing the determination of the level of expression of a marker, are those described by Sambrook et al. (1989) or real time methods known in the art as the TaqMan® method disclosed in WO92/02638 and the corresponding U.S. 5,210,015, U.S. 5,804,375, U.S. 5,487,972. This method exploits the exonuclease activity of a polymerase to generate a signal. In detail, the (at least one) target nucleic acid component is detected by a process comprising contacting the sample with an oligonucleotide containing a sequence complementary to a region of the target nucleic acid component and a labeled oligonucleotide containing a sequence complementary to a second region of the same target nucleic acid component sequence strand, but not including the nucleic acid sequence defined by the first oligonucleotide, to create a mixture of duplexes during hybridization conditions, wherein the duplexes comprise the target nucleic acid annealed to the first oligonucleotide and to the labeled oligonucleotide such that the 3'-end of the first oligonucleotide is adjacent to the 5'-end of the labeled oligonucleotide. Then this mixture is treated with a template-dependent nucleic acid polymerase having a 5' to 3' nuclease activity under conditions sufficient to permit the 5' to 3' nuclease activity of the polymerase to cleave the annealed, labeled oligonucleotide and release labeled fragments. The signal generated by the hydrolysis of the labeled oligonucleotide is detected and/ or measured. TaqMan® technology eliminates the

need for a solid phase bound reaction complex to be formed and made detectable. Other methods include e.g. fluorescence resonance energy transfer between two adjacently hybridized probes as used in the LightCycler® format described in U.S. 6,174,670.

A preferred protocol if the marker, i.e. the polynucleotide, is in form of a transcribed nucleotide, is described in Example 3, where total RNA is isolated, cDNA and, subsequently, cRNA is synthesized and biotin is incorporated during the transcription reaction. The purified cRNA is applied to commercially available arrays which can be obtained e.g. from Affymetrix. The hybridized cRNA is detected according to the methods described in Example 3. The arrays are produced by photolithography or other methods known to experts skilled in the art e.g. from U.S. 5,445,934, U.S. 5,744,305, U.S. 5,700,637, U.S. 5,945,334 and EP 0 619 321 or EP 0 373 203, or as decribed hereinafter in greater detail.

In another embodiment of the present invention, the polynucleotide or at least one of the polynucleotides is in form of a polypeptide. In another preferred embodiment, the expression level of the polynucleotides or polypeptides is detected using a compound which specifically binds to the polynucleotide of the polypeptide of the present invention.

As used herein, "specifically binding" means that the compound is capable of discriminating between two or more polynucleotides or polypeptides, i.e. it binds to the desired polynucleotide or polypeptide, but essentially does not bind unspecifically to a different polynucleotide or polypeptide.

The compound can be an antibody, or a fragment thereof, an enzyme, a so-called small molecule compound, a protein-scaffold, preferably an anticalin. In a preferred embodiment, the compound specifically binding to the polynucleotide or polypeptide is an antibody, or a fragment thereof.

As used herein, an "antibody" comprises monoclonal antibodies as first described by Köhler and Milstein in Nature 278 (1975), 495-497 as well as polyclonal antibodies, i.e. entibodies contained in a polyclonal antiserum. Monoclonal antibodies include those produced by transgenic mice. Fragments of antibodies

include $F(ab')_2$, Fab and Fv fragments. Derivatives of antibodies include scFvs, chimeric and humanized antibodies. See, for example Harlow and Lane, loc. cit. For the detection of polypeptides using antibodies or fragments thereof, the person skilled in the art is aware of a variety of methods, all of which are included in the present invention. Examples include immunoprecipitation, Western blotting, Enzyme-linked immuno sorbent assay (ELISA), Enzyme-linked immuno sorbent assay (RIA), dissociation-enhanced lanthanide fluoro immuno assay (DELFIA), scintillation proximity assay (SPA). For detection, it is desirable if the antibody is labelled by one of the labelling compounds and methods described supra.

In another preferred embodiment of the present invention, the method for distinguishing MLL-PTD-positive AML from other AML subtypes is carried out on an array.

In general, an "array" or "microarray" refers to a linear or two- or three dimensional arrangement of preferably discrete nucleic acid or polypeptide probes which comprises an intentionally created collection of nucleic acid or polypeptide probes of any length spotted onto a substrate/solid support. The person skilled in the art knows a collection of nucleic acids or polypeptide spotted onto a substrate/solid support also under the term "array". As known to the person skilled in the art, a microarray usually refers to a miniaturised array arrangement, with the probes being attached to a density of at least about 10, 20, 50, 100 nucleic acid molecules referring to different or the same genes per cm^2. Furthermore, where appropriate an array can be referred to as "gene chip". The array itself can have different formats, e.g. libraries of soluble probes or libraries of probes tethered to resin beads, silica chips, or other solid supports.

The process of array fabrication is well-known to the person skilled in the art. In the following, the process for preparing a nucleic acid array is described. Commonly, the process comprises preparing a glass (or other) slide (e.g. chemical treatment of the glass to enhance binding of the nucleic acid probes to the glass surface), obtaining DNA sequences representing genes of a genome of interest, and spotting sequences these sequences of interest onto glass slide. Sequences of interest can be obtained via creating a cDNA library from an mRNA source or by using publicly available databases, such as GeneBank, to annotate the sequence

information of custom cDNA libraries or to identify cDNA clones from previously prepared libraries. Generally, it is recommendable to amplify obtained sequences by PCR in order to have sufficient amounts of DNA to print on the array. The liquid containing the amplified probes can be deposited on the array by using a set of microspotting pins. Ideally, the amount deposited should be uniform. The process can further include UV-crosslinking in order to enhance immobilization of the probes on the array.

In a preferred embodiment, the array is a high density oligonucleotide (oligo) array using a light-directed chemical synthesis process, employing the so-called photolithography technology. Unlike common cDNA arrays, oligo arrays (according to the Affymetrix technology) use a single-dye technology. Given the sequence information of the markers, the sequence can be synthesized directly onto the array, thus, bypassing the need for physical intermediates, such as PCR products, required for making cDNA arrays. For this purpose, the marker, or partial sequences thereof, can be represented by 14 to 20 features, preferably by less than 14 features, more preferably less than 10 features, even more preferably by 6 features or less, with each feature being a short sequence of nucleotides (oligonucleotide), which is a perfect match (PM) to a segment of the respective gene. The PM oligonucleotide are paired with mismatch (MM) oligonucleotides which have a single mismatch at the central base of the nucleotide and are used as "controls". The chip exposure sites are defined by masks and are deprotected by the use of light, followed by a chemical coupling step resulting in the synthesis of one nucleotide. The masking, light deprotection, and coupling process can then be repeated to synthesize the next nucleotide, until the nucleotide chain is of the specified length.

Advantageously, the method of the present invention is carried out in a robotics system including robotic plating and a robotic liquid transfer system, e.g. using microfluidics, i.e. channelled structured.

A particular preferred method according to the present invention is as follows:

1. Obtaining a sample, e.g. bone marrow aliquots, from a patient having AML
2. Extracting RNA, preferably mRNA, from the sample
3. Reverse transcribing the RNA into cDNA
4. In vitro transcribing the cDNA into cRNA
5. Fragmenting the cRNA

6. Hybridizing the fragmented cRNA on standard microarrays
7. Determining hybridization

In another embodiment, the present invention is directed to the use of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, and/or 3, for the manufacturing of a diagnostic for distinguishing MLL-PTD-positive AML from other AML subtypes. The use of the present invention is particularly advantageous for distinguishing MLL-PTD-positive AML from other AML subtypes in an individual having AML. The use of said markers for diagnosis of MLL-PTD-positive AML, preferably based on microarray technology, offers the following advantages: (1) more rapid and more precise diagnosis, (2) easy to use in laboratories without specialized experience, (3) abolishes the requirement for analyzing viable cells for chromosome analysis (transport problem), and (4) very experienced hematologists for cytomorphology and cytochemistry, immunophenotyping as well as cytogeneticists and molecularbiologists are no longer required.

Accordingly, the present invention refers to a diagnostic kit containing at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 3 for distinguishing MLL-PTD-positive AML from other AML subtypes, in combination with suitable auxiliaries. Suitable auxiliaries, as used herein, include buffers, enzymes, labelling compounds, and the like. In a preferred embodiment, the marker contained in the kit is a nucleic acid molecule which is capable of hybridizing to the mRNA corresponding to at least one marker of the present invention. Preferably, the at least one nucleic acid molecule is attached to a solid support, e.g. a polystyrene microtiter dish, nitrocellulose membrane, glass surface or to non-immobilized particles in solution.

In another preferred embodiment, the diagnostic kit contains at least one reference for a MLL-PTD-positive AML subtype. As used herein, the reference can be a sample or a data bank.

In another embodiment, the present invention is directed to an apparatus for distinguishing MLL-PTD-positive AML from other AML subtypes in a sample, containing a reference data bank obtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level at least one marker selected from the markers

identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 3, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

According to the present invention, the "machine learning algorithm" is a computational-based prediction methodology, also known to the person skilled in the art as "classifier", employed for characterizing a gene expression profile. The signals corresponding to a certain expression level which are obtained by the microarray hybridization are subjected to the algorithm in order to classify the expression profile. Supervised learning involves "training" a classifier to recognize the distinctions among classes and then "testing" the accuracy of the classifier on an independent test set. For new, unknown sample the classifier shall predict into which class the sample belongs.

Preferably, the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines (SVM), and Feed-Forward Neural Networks. Most preferably, the machine learning algorithm is Support Vector Machine, such as polynomial kernel and Gaussian Radial Basis Function-kernel SVM models.

The classification accuracy of a given gene list for a set of microarray experiments is preferably estimated using Support Vector Machines (SVM), because there is evidence that SVM-based prediction slightly outperforms other classification techniques like k-Nearest Neighbors (k-NN). The LIBSVM software package version 2.36 was used (SVM-type: C-SVC, linear kernel (http://www.csie.ntu.edu.tw/~cjlin/libsvm/)). The skilled artisan is furthermore referred to Brown et al., Proc.Natl.Acad.Sci., 2000; 97: 262-267, Furey et al., Bioinformatics. 2000; 16: 906-914, and Vapnik V. Statistical Learning Theory. New York: Wiley, 1998.

In detail, the classification accuracy of a given gene list for a set of microarray experiments can be estimated using Support Vector Machines (SVM) as supervised learning technique. Generally, SVMs are trained using differentially expressed genes which were identified on a subset of the data and then this trained model is employed to assign new samples to those trained groups from a second and

different data set. Differentially expressed genes were identified applying ANOVA and t-test-statistics (Welch t-test). Based on identified distinct gene expression signatures respective training sets consisting of 2/3 of cases and test sets with 1/3 of cases to assess classification accuracies are designated. Assignment of cases to training and test set is randomized and balanced by diagnosis. Based on the training set a Support Vector Machine (SVM) model is built.

According to the present invention, the apparent accuracy, i.e. the overall rate of correct predictions of the complete data set was estimated by 10fold cross validation. This means that the data set was divided into 10 approximately equally sized subsets, an SVM-model was trained for 9 subsets and predictions were generated for the remaining subset. This training and prediction process was repeated 10 times to include predictions for each subset. Subsequently the data set was split into a training set, consisting of two thirds of the samples, and a test set with the remaining one third. Apparent accuracy for the training set was estimated by 10fold cross validation (analogous to apparent accuracy for complete set). A SVM-model of the training set was built to predict diagnosis in the independent test set, thereby estimating true accuracy of the prediction model. This prediction approach was applied both for overall classification (multi-class) and binary classification (diagnosis X => yes or no). For the latter, sensitivity and specificity were calculated:

Sensitivity = (number of positive samples predicted)/(number of true positives)

Specificity = (number of negative samples predicted)/(number of true negatives)

In a preferred embodiment, the reference data bank is backed up on a computational data memory chip which can be inserted in as well as removed from the apparatus of the present invention, e.g. like an interchangeable module, in order to use another data memory chip containing a different reference data bank.

The apparatus of the present invention containing a desired reference data bank can be used in a way such that an unknown sample is, first, subjected to gene expression profiling, e.g. by microarray analysis in a manner as described supra or in the art, and the expression level data obtained by the analysis are, second, fed into the apparatus and compared with the data of the reference data bank obtainable by the above method. For this purpose, the apparatus suitably contains a device for

entering the expression level of the data, for example a control panel such as a keyboard. The results, whether and how the data of the unknown sample fit into the reference data bank can be made visible on a provided monitor or display screen and, if desired, printed out on an incorporated of connected printer.

Alternatively, the apparatus of the present invention is equipped with particular appliances suitable for detecting and measuring the expression profile data and, subsequently, proceeding with the comparison with the reference data bank. In this embodiment, the apparatus of the present invention can contain a gripper arm and/or a tray which takes up the microarray containing the hybridized nucleic acids.

In another embodiment, the present invention refers to a reference data bank for distinguishing MLL-PTD-positive AML from other AML subtypes in a sample obtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 3, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

Preferably, the reference data bank is backed up and/or contained in a computational memory data chip.

The invention is further illustrated in the following table and examples, without limiting the scope of the invention:

TABLE 1.1-3.15

Table 1.1-3.15 show AML subtype analysis of MLL-PTD-positive AML versus other AML subtypes. The analysed markers are ordered according to their q-values, beginning with the lowest q-values.

For convenience and a better understanding, Tables 1.1 to 3.15 are accompanied with explanatory tables (Table 1.1A to 3.15A) where the numbering and the Affymetrix Id are further defined by other parameters, e.g. gene bank accession number.

EXAMPLES

Example 1: General experimental design of the invention and results

Partial tandem duplication within the MLL-gene (MLL-PTD) can be found in 10% of AML with normal karyotype. Like MLL-translocations (t(11q23)/MLL) the occurence of MLL-PTD is characterized by an unfavourable prognosis. The pathogenetic mechanisms of the MLL-PTD are poorly understood and downstream genes effected by this molecular aberration are not known. To get more insight into the pathogenesis of PTD+ AML we performed global gene expression profiling of 184 AML samples at diagnosis using the U133 set of expression microarrays (Affymetrix) with >30,000 human genes represented on both arrays. Microarray data was analyzed by pattern recognition algorithms (Principal Component Analysis (PCA), hierarchical clustering), as well as Support Vector Machines (SVM) for estimation of classification accuracies. Therefore, all samples were divided into a training set consisting of 2/3 of cases to built a SVM model and a test set with remaining 1/3 of cases. Assignment of cases to training and test set was randomized and balanced by diagnosis. Differentially expressed genes were selected according to ANOVA and t-test-statistics in the training set. Classification accuracy was assessed in the test set. In detail, we analyzed 30 cases with t(11q23)/MLL, 30 cases with normal karyotype AML and MLL-PTD (PTD+ AML) and 124 cases with normal karyotype without MLL-PTD (AML-NK). All data analysis algorithms demonstrate that PTD+ AML can clearly be distinguished from t(11q23)/MLL positive AML with 100% accuracy. Thus, despite an identical gene targeted by molecular mutation or chromosomal translocation, this finding illustrates that both kinds of aberrations lead to biologically distinct leukemia subclasses. Some of the most significantly differentially expressed genes that were highly expressed in t(11q23)/MLL in comparison to PTD+ AML were CACNA2DA, MBNL1, and PBX3. Reversely, genes with high expression in PTD+ and low in t(11q23)/MLL samples were HOXB5, HOXB2, MAN1A1, and ZNF207. At next, we addressed the question whether PTD+ AML can be discriminated from AML-NK by a specific gene expression signature. Both PCA and hierarchical cluster visualize that the MLL-PTD samples characterize a homogeneous subgroup within AML with normal karyotype, but do not separate from them. Some of the genes that were highly expressed in AML-NK and low in PTD+ were AAK1, RAB4A, HOXA2, BID. On the other hand genes that were low

in AML-NK and high in PTD+ were, among others, MLL, YY1, and SRP46. In addition, we attempted to classify the analyzed samples by means of SVM. Here, the training set comprised 83 AML-NK and 19 PTD+ AML cases, the test set 41 AML-NK and 9 PTD+ AML cases, respectively. The 50 test samples were assigned to the correct group with an accuracy of 88%. In detail, 6/9 PTD+ AML (92.7% specificity, 66.7% sensitivity) and 38/41 AML-NK (66.7% specificity, 92.7% sensitivity) were accurately assigned. In conclusion, despite a significantly worse prognosis of the PTD+ AML cases within the large group of AML with normal karyotype it is not possible to designate a highly characteristic specific gene expression signature at diagnosis as has been demonstrated for AML with balanced chromosomal aberrations. This unexpected results may be in part due to the fact that pts with PTD do not belong to a specific morphologic subgroup. Thus the expression pattern associated with heterogenous FAB subtypes may overwrite that generated bei the PTD. In addition, different unknown accompanying mutation may generate a dominant expression pattern.

Example 2: General materials, methods and definitions of functional annotations

The methods section contains both information on statistical analyses used for identification of differentially expressed genes and detailed annotation data of identified microarray probesets.

Affymetrix Probeset Annotation

All annotation data of GeneChip® arrays are extracted from the NetAffx™ Analysis Center (internet website: www.affymetrix.com). Files for U133 set arrays, including U133A and U133B microarrays are derived from the June 2003 release. The original publication refers to: Liu G, Loraine AE, Shigeta R, Cline M, Cheng J, Valmeekam V, Sun S, Kulp D, Siani-Rose MA. NetAffx: Affymetrix probesets and annotations. Nucleic Acids Res. 2003;31(1):82-6.

The sequence data are omitted due to their large size, and because they do not change, whereas the annotation data are updated periodically, for example new information on chromomal location and functional annotation of the respective gene products. Sequence data are available for download in the NetAffx Download Center (www.affymetrix.com)

Data fields:

In the following section, the content of each field of the data files are described. Microarray probesets, for example found to be differentially expressed between different types of leukemia samples are further described by additional information. The fields are of the following types:

1. GeneChip Array Information
2. Probe Design Information
3. Public Domain and Genomic References

1. GeneChip Array Information

HG-U133 ProbeSet_ID:

HG-U133 ProbeSet_ID describes the probe set identifier. Examples are: 200007_at, 200011_s_at, 200012_x_at.

GeneChip:

The description of the GeneChip probe array name where the respective probeset is represented. Examples are: Affymetrix Human Genome U133A Array or Affymetrix Human Genome U133B Array.

2. Probe Design Information

Sequence Type:

The Sequence Type indicates whether the sequence is an Exemplar, Consensus or Control sequence. An Exemplar is a single nucleotide sequence taken directly from a public database. This sequence could be an mRNA or EST. A Consensus sequence, is a nucleotide sequence assembled by Affymetrix, based on one or more sequence taken from a public database.

Transcript ID:

The cluster identification number with a sub-cluster identifier appended.

Sequence Derived From:

The accession number of the single sequence, or representative sequence on which the probe set is based. Refer to the "Sequence Source" field to determine the database used.

Sequence ID:
For Exemplar sequences: Public accession number or GenBank identifier. For Consensus sequences: Affymetrix identification number or public accession number.

Sequence Source:
The database from which the sequence used to design this probe set was taken. Examples are: GenBank®, RefSeq, UniGene, TIGR (annotations from The Institute for Genomic Research).

3. Public Domain and Genomic References

Most of the data in this section come from LocusLink and UniGene databases, and are annotations of the reference sequence on which the probe set is modeled.

Gene Symbol and Title:
A gene symbol and a short title, when one is available. Such symbols are assigned by different organizations for different species. Affymetrix annotational data come from the UniGene record. There is no indication which species-specific databank was used, but some of the possibilities include for example HUGO: The Human Genome Organization.

MapLocation:
The map location describes the chromosomal location when one is available.

Unigene_Accession:
UniGene accession number and cluster type. Cluster type can be "full length" or "est", or "---" if unknown.

LocusLink:
This information represents the LocusLink accession number.

Full Length Ref. Sequences:
Indicates the references to multiple sequences in RefSeq. The field contains the ID and description for each entry, and there can be multiple entries per probeSet.

Example 3: Sample preparation, processing and data analysis

Method 1:

Microarray analyses were performed utilizing the GeneChip® System (Affymetrix, Santa Clara, USA). Hybridization target preparations were performed according to recommended protocols (Affymetrix Technical Manual). In detail, at time of diagnosis, mononuclear cells were purified by Ficoll-Hypaque density centrifugation. They had been lysed immediately in RLT buffer (Qiagen, Hilden, Germany), frozen, and stored at -80°C from 1 week to 38 months. For gene expression profiling cell lysates of the leukemia samples were thawed, homogenized (QIAshredder, Qiagen), and total RNA was extracted (RNeasy Mini Kit, Qiagen). Subsequently, 5-10 µg total RNA isolated from 1 x 10^7 cells was used as starting material for cDNA synthesis with oligo$[(dT)_{24}T7promotor]_{65}$ primer (cDNA Synthesis System, Roche Applied Science, Mannheim, Germany). cDNA products were purified by phenol/chlorophorm/IAA extraction (Ambion, Austin, USA) and acetate/ethanol-precipitated overnight. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides were incorporated during the following *in vitro* transcription reaction (Enzo BioArray HighYield RNA Transcript Labeling Kit, Enzo Diagnostics). After quantification by spectrophotometric measurements and 260/280 absorbance values assessment for quality control of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 µg cRNA was fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2/500 mM potassium acetate/150 mM magnesium acetate) and added to the hybridization cocktail sufficient for five hybridizations on standard GeneChip microarrays (300 µl final volume). Washing and staining of the probe arrays was performed according to the recommended Fluidics Station protocol (EukGE-WS2v4). Affymetrix Microarray Suite software (version 5.0.1) extracted fluorescence signal intensities from each feature on the microarrays as detected by confocal laser scanning according to the manufacturer's recommendations.

Expression analysis quality assessment parameters included visiual array inspection of the scanned image for the presence of image artifacts and correct grid

alignment for the identification of distinct probe cells as well as both low 3'/5' ratio of housekeeping controls (mean: 1.90 for GAPDH) and high percentage of detection calls (mean: 46.3% present called genes). The 3' to 5' ratio of GAPDH probesets can be used to assess RNA sample and assay quality. Signal values of the 3' probe sets for GAPDH are compared to the Signal values of the corresponding 5' probe set. The ratio of the 3' probe set to the 5' probe set is generally no more than 3.0. A high 3' to 5' ratio may indicate degraded RNA or inefficient synthesis of ds cDNA or biotinylated cRNA (GeneChip® Expression Analysis Technical Manual, www.affymetrix.com). Detection calls are used to determine whether the transcript of a gene is detected (present) or undetected (absent) and were calculated using default parameters of the Microarray Analysis Suite MAS 5.0 software package.

Method 2:

Bone marrow (BM) aspirates are taken at the time of the initial diagnostic biopsy and remaining material is immediately lysed in RLT buffer (Qiagen), frozen and stored at -80 C until preparation for gene expression analysis. For microarray analysis the GeneChip System (Affymetrix, Santa Clara, CA, USA) is used. The targets for GeneChip analysis are prepared according to the current Expression Analysis. Briefly, frozen lysates of the leukemia samples are thawed, homogenized (QIAshredder, Qiagen) and total RNA extracted (RNeasy Mini Kit, Qiagen).Normally 10 ug total RNA isolated from 1 x 107 cells is used as starting material in the subsequent cDNA-Synthesis using Oligo-dT-T7-Promotor Primer (cDNA synthesis Kit, Roche Molecular Biochemicals). The cDNA is purified by phenol-chlorophorm extraction and precipitated with 100% Ethanol over night. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides are incorporated during the in vitro transcription reaction (Enzo® BioArray™ HighYield™ RNA Transcript Labeling Kit, ENZO). After quantification of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 ug are fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2, 500 mM potassium acetate, 150 mM magnesium acetate) and added to the hybridization cocktail sufficient for 5 hybridizations on standard GeneChip microarrays. Before expression profiling Test3 Probe Arrays (Affymetrix) are chosen for monitoring of the integrity of the cRNA. Only labeled cRNA-cocktails which showed a ratio of the messured intensity of the 3' to the 5' end of the GAPDH gene less than 3.0 are selected for subsequent hybridization on HG-U133 probe arrays (Affymetrix). Washing and

staining the Probe arrays is performed as described (siehe Affymetrix-Original-Literatur (LOCKHART und LIPSHUTZ). The Affymetrix software (Microarray Suite, Version 4.0.1) extracted fluorescence intensities from each element on the arrays as detected by confocal laser scanning according to the manufacturers recommendations.

Table 1

1. One-Versus-All (OVA)								
1.1	normal mit MLL-PTD versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205434_s_at	AAK1	-1.73	1.11E-12	3.44E-08	-0.71	-8.05	2p24.3-p14
2	226678_at		-2.48	2.72E-11	4.24E-07	-0.67	-7.47	
3	210150_s_at	LAMA5	-2.40	4.29E-11	4.45E-07	-0.66	-7.41	20q13.2-q13.3
4	203582_s_at	RAB4A	-1.60	2.57E-08	1.02E-04	-0.67	-6.66	1q42-q43
5	204069_at	MEIS1	-2.43	7.65E-09	5.95E-05	-0.56	-6.29	2p14-p13
6	205180_s_at	ADAM8	-2.33	6.23E-08	1.49E-04	-0.59	-6.18	10q26.3
7	233268_s_at	SELENBP1	-1.51	4.14E-08	1.17E-04	-0.57	-6.15	1q21-q22
8	236893_at		-3.17	1.35E-08	8.43E-05	-0.53	-6.06	
9	228042_at	ADPRH	-2.92	2.62E-08	1.02E-04	-0.54	-6.02	3q13.31-q13.33
10	236892_s_at		-2.39	3.66E-08	1.14E-04	-0.54	-5.99	
11	214455_at	HIST1H2BC	-2.82	2.07E-08	1.02E-04	-0.52	-5.98	6p21.3
12	211979_at	GPR107	-1.76	4.12E-07	5.01E-04	-0.61	-5.97	9q34.13
13	224461_s_at	AMID	-2.75	2.95E-08	1.02E-04	-0.51	-5.91	10q22.1
14	211075_s_at	CD47	-1.58	2.53E-07	4.37E-04	-0.57	-5.87	3q13.1-q13.2
15	209907_s_at	ITSN2	-1.39	7.23E-08	1.61E-04	-0.53	-5.85	2pter-p25.1
16	228083_at	CACNA2D4	-3.83	5.92E-08	1.49E-04	-0.50	-5.76	12p13.33
17	217497_at	ECGF1	-2.29	9.40E-08	1.95E-04	-0.51	-5.73	22q13.33
18	239791_at		-2.32	1.56E-07	3.04E-04	-0.52	-5.70	
19	225522_at		-1.54	5.65E-07	5.86E-04	-0.54	-5.64	
20	219696_at	FLJ20054	-1.56	3.93E-07	5.01E-04	-0.52	-5.60	1q31.1
21	224318_s_at	FLJ10081	-1.26	3.12E-07	4.60E-04	-0.51	-5.59	2p12-p11.2
22	227043_at		-2.52	2.76E-07	4.52E-04	-0.50	-5.56	
23	229001_at	LOC90673	-3.14	3.25E-07	4.60E-04	-0.50	-5.50	14q11.2
24	237791_at		-1.93	2.10E-07	3.85E-04	-0.48	-5.50	
25	205270_s_at	LCP2	-1.64	8.19E-07	7.97E-04	-0.52	-5.48	5q33.1-qter
26	227575_s_at	C14orf102	-1.52	4.34E-07	5.01E-04	-0.49	-5.46	14q32.11
27	219634_at	C4ST	-1.43	9.62E-07	8.56E-04	-0.52	-5.44	12q
28	208284_x_at	GGT1	-1.80	3.21E-07	4.60E-04	-0.48	-5.43	22q11.23
29	201048_x_at	RAB6A	-1.68	1.54E-06	1.11E-03	-0.53	-5.40	11q13.3
30	227711_at	FLJ32942	-2.70	9.56E-07	8.56E-04	-0.51	-5.40	12q13.13
31	225402_at	C20orf64	-1.44	7.03E-07	7.06E-04	-0.49	-5.39	
32	203052_at	C2	-2.86	3.67E-07	4.96E-04	-0.47	-5.38	6p21.3
33	227186_s_at	MRPL41	-1.54	1.67E-06	1.15E-03	-0.51	-5.34	9q34.3
34	239762_at		-1.87	4.32E-07	5.01E-04	-0.47	-5.33	
35	210549_s_at	CCL23	-3.69	4.98E-07	5.54E-04	-0.47	-5.33	17q12
36	204082_at	PBX3	-1.88	1.25E-06	9.99E-04	-0.50	-5.32	9q33-q34
37	226872_at	RFX2	-1.86	5.60E-07	5.86E-04	-0.47	-5.31	19p13.3-p13.2
38	204493_at	BID	-1.76	2.02E-06	1.31E-03	-0.52	-5.31	22q11.1
39	202135_s_at	ACTR1B	-1.41	2.28E-06	1.36E-03	-0.51	-5.28	2q11.1-q11.2
40	201328_at		-1.89	1.39E-06	1.06E-03	-0.49	-5.27	

41	214457_at	HOXA2	-2.49	1.16E-06	9.49E-04	-0.48	-5.24	7p15-p14
42	227325_at		-1.36	2.65E-06	1.53E-03	-0.49	-5.18	
43	205329_s_at	SNX4	-1.52	3.00E-06	1.61E-03	-0.49	-5.16	3q21.2
44	202271_at	KIAA0483	-1.50	1.62E-06	1.14E-03	-0.47	-5.16	1q42.12
45	210548_at	CCL23	-2.54	9.39E-07	8.56E-04	-0.45	-5.15	17q12
46	229607_at	BTBD2	-2.06	9.93E-07	8.59E-04	-0.45	-5.14	19p13.3
47	226542_at		-1.39	1.13E-06	9.49E-04	-0.45	-5.12	
48	215997_s_at	CUL4B	-1.35	5.73E-06	2.29E-03	-0.51	-5.11	Xq23
49	218749_s_at	FLJ22233	-1.57	7.09E-06	2.51E-03	-0.52	-5.10	12q24.21
50	221560_at	MARK4	-1.71	1.34E-06	1.04E-03	-0.45	-5.10	19q13.3

Table 2

One-Versus-All (OVA)

2.1	M4eo versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	227567_at		-4.48	6.22E-27	2.03E-22	-1.28	-14.30	
2	225055_at	DKFZp667M2411	-4.49	3.38E-25	5.49E-21	-1.17	-13.20	17q11.2
3	202370_s_at	CBFB	-2.56	1.56E-24	1.69E-20	-1.14	-12.87	16q22.1
4	224952_at	DKFZP564D166	-3.65	6.41E-20	3.48E-16	-1.13	-12.19	17q23.3
5	213737_x_at		-2.48	1.29E-21	1.05E-17	-1.03	-11.61	
6	225102_at	LOC152009	-4.29	1.14E-20	7.43E-17	-0.99	-11.23	3q21.3
7	200675_at	CD81	-3.06	8.04E-18	2.01E-14	-1.03	-11.10	11p15.5
8	228497_at	FLIPT1	-5.34	1.08E-19	5.02E-16	-0.99	-11.00	1p13.1
9	232636_at	DKFZp547M2010	-10.08	7.75E-19	2.45E-15	-1.00	-10.80	Xq27.3
10	201497_x_at	MYH11	23.26	1.74E-10	5.01E-08	2.10	10.80	16p13.13-p13.12
11	218414_s_at	NUDE1	-1.97	4.45E-19	1.61E-15	-0.96	-10.72	16p13.11
12	227224_at	FLJ25604	-3.78	9.88E-18	2.30E-14	-0.98	-10.71	1q24.2
13	201496_x_at	MYH11	6.33	1.25E-10	3.87E-08	1.61	10.61	16p13.13-p13.12
14	226352_at		-5.04	4.28E-19	1.61E-15	-0.94	-10.60	
15	223471_at	RAB3IP	-3.03	9.41E-19	2.55E-15	-0.94	-10.59	
16	229215_at	ASCL2	-6.63	8.28E-19	2.45E-15	-0.93	-10.51	11p15.5
17	200665_s_at	SPARC	3.56	3.52E-11	1.29E-08	1.21	10.02	5q31.3-q32
18	218795_at	ACP6	-3.22	1.16E-16	2.21E-13	-0.90	-9.97	1q21
19	204197_s_at	RUNX3	-3.13	4.00E-17	8.68E-14	-0.86	-9.77	1p36
20	219379_x_at	ZNF358	-3.06	1.42E-16	2.57E-13	-0.86	-9.67	
21	204198_s_at	RUNX3	-4.01	1.57E-16	2.69E-13	-0.86	-9.65	1p36
22	219218_at	FLJ23058	-4.37	8.57E-17	1.74E-13	-0.85	-9.64	17q25.3
23	211031_s_at	CYLN2	-6.83	2.15E-16	3.49E-13	-0.87	-9.63	7q11.23
24	203973_s_at	CEBPD	2.24	1.61E-12	8.71E-10	0.99	9.63	8p11.2-p11.1
25	231310_at		2.58	6.79E-12	3.07E-09	1.01	9.52	
26	242520_s_at		-4.60	5.45E-16	8.06E-13	-0.85	-9.45	
27	213779_at	LOC129080	-3.31	3.60E-16	5.59E-13	-0.83	-9.40	22q12.1
28	222786_at	C4S-2	-2.73	8.62E-16	1.22E-12	-0.82	-9.23	7p22
29	201432_at	CAT	-1.88	8.68E-14	7.06E-11	-0.86	-9.14	11p13
30	227533_at		-2.35	1.62E-14	1.82E-11	-0.83	-9.11	
31	211026_s_at	MGLL	-2.35	2.82E-15	3.83E-12	-0.80	-9.04	3q21.3
32	227856_at	FLJ39370	-4.04	4.68E-15	6.09E-12	-0.81	-9.03	4q25
33	201669_s_at	MARCKS	-8.16	8.93E-15	1.12E-11	-0.80	-8.92	6q22.2
34	200984_s_at	CD59	-2.75	1.08E-14	1.25E-11	-0.78	-8.81	11p13
35	200985_s_at	CD59	-5.71	1.04E-14	1.25E-11	-0.78	-8.78	11p13
36	220668_s_at	DNMT3B	-2.74	1.79E-14	1.94E-11	-0.77	-8.67	20q11.2
37	238365_s_at		-4.42	4.30E-14	4.12E-11	-0.78	-8.64	

38	213908_at		-7.27	5.16E-14	4.59E-11	-0.79	-8.62	
39	230728_at		-3.92	4.27E-14	4.12E-11	-0.77	-8.62	
40	241985_at	FLJ37870	-4.89	2.54E-14	2.66E-11	-0.76	-8.61	5q13.3
41	207075_at	CIAS1	2.67	3.52E-10	9.33E-08	0.97	8.61	1q44
42	213915_at	NKG7	-2.87	3.00E-14	3.05E-11	-0.76	-8.61	19q13.33
43	224724_at	SULF2	5.74	4.86E-09	8.19E-07	1.20	8.59	20q12-13.2
44	214651_s_at	HOXA9	-11.40	8.17E-14	6.82E-11	-0.78	-8.55	7p15-p14
45	227929_at		-8.81	7.13E-14	6.11E-11	-0.77	-8.54	
46	205419_at	EBI2	2.88	7.89E-10	1.81E-07	0.99	8.54	13q32.2
47	230894_s_at		-6.89	4.65E-14	4.33E-11	-0.75	-8.50	
48	223044_at	SLC11A3	-6.02	5.22E-14	4.59E-11	-0.75	-8.48	2q32
49	218477_at	PTD011	-2.45	1.30E-13	9.87E-11	-0.75	-8.38	6p12.1
50	212463_at		-3.96	1.08E-13	8.58E-11	-0.74	-8.38	
2.2	PTD versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	AFFX-HSAC07/X00351_M_at - HG-U133B	ACTB	-1.79	2.83E-10	5.20E-07	-0.80	-7.93	7p15-p12
2	200885_at	ARHC	-2.26	3.49E-12	4.17E-08	-0.72	-7.92	1p13.1
3	205131_x_at	SCGF	-4.34	1.66E-12	3.97E-08	-0.69	-7.85	19q13.3
4	208623_s_at	VIL2	-2.26	3.72E-11	1.33E-07	-0.74	-7.81	6q25.2-q26
5	205600_x_at	HOXB5	2.65	1.37E-07	3.63E-05	1.24	7.61	17q21.3
6	210783_x_at	SCGF	-4.02	8.51E-12	6.78E-08	-0.67	-7.54	19q13.3
7	208858_s_at	MBC2	-2.31	5.02E-11	1.33E-07	-0.69	-7.49	12q13.13
8	220363_s_at	ELMO2	-4.14	1.34E-11	7.98E-08	-0.66	-7.45	20q13
9	224659_at	SEPN1	-2.56	7.93E-10	1.01E-06	-0.73	-7.42	1p36.13
10	218530_at	FHOD1	-1.64	4.86E-11	1.33E-07	-0.66	-7.35	16q22
11	209679_s_at	LOC57228	-2.47	5.02E-10	7.50E-07	-0.70	-7.34	12q13.12
12	203331_s_at	INPP5D	-2.87	3.72E-11	1.33E-07	-0.66	-7.34	2q36-q37
13	205601_s_at	HOXB5	3.02	2.74E-07	5.85E-05	1.19	7.29	17q21.3
14	210213_s_at	ITGB4BP	-1.69	2.12E-10	4.61E-07	-0.67	-7.26	20q12
15	225065_x_at	MGC40157	-2.21	4.24E-11	1.33E-07	-0.64	-7.23	17p11.2
16	227711_at	FLJ32942	-3.24	8.04E-10	1.01E-06	-0.69	-7.20	12q13.13
17	203332_s_at	INPP5D	-1.59	1.44E-09	1.43E-06	-0.67	-7.06	2q36-q37
18	214789_x_at	SRP46	1.67	8.09E-09	5.54E-06	0.72	7.05	11q22
19	AFFX-HSAC07/X00351_M_at - HG-U133A	ACTB	-1.72	1.41E-08	8.14E-06	-0.74	-7.04	7p15-p12
20	201043_s_at	ANP32A	-2.54	4.44E-10	7.07E-07	-0.63	-6.95	15q22.3-q23
21	201389_at	ITGA5	-1.80	2.09E-10	4.61E-07	-0.61	-6.92	12q11-q13
22	207106_s_at	LTK	-2.46	2.45E-10	4.89E-07	-0.61	-6.90	15q15.1-q21.1
23	208072_s_at	DGKD	-1.99	1.14E-09	1.30E-06	-0.63	-6.85	2q37.1
24	211709_s_at	SCGF	-2.48	1.74E-08	9.22E-06	-0.69	-6.81	19q13.3
25	213048_s_at	SET	-1.78	4.29E-10	7.07E-07	-0.61	-6.81	9q34

26	200982_s_at	ANXA6	-2.26	2.79E-09	2.47E-06	-0.64	-6.81	5q32-q34
27	229143_at	CNOT3	1.81	2.88E-07	6.03E-05	0.86	6.80	19q13.4
28	227564_at	FLJ32731	-2.59	5.94E-10	8.35E-07	-0.60	-6.73	8p11.1
29	213159_at	PCNX	-2.06	2.67E-08	1.19E-05	-0.69	-6.73	14q24.1
30	209406_at	BAG2	2.62	2.93E-07	6.03E-05	0.82	6.68	6p12.3-p11.2
31	217223_s_at	BCR	-2.04	1.40E-09	1.43E-06	-0.60	-6.68	22q11.23
32	221879_at	MGC4809	-2.49	7.52E-09	5.45E-06	-0.64	-6.67	15q22.2
33	201005_at	CD9	-3.85	3.17E-09	2.70E-06	-0.61	-6.64	12p13.3
34	226678_at		-2.50	1.06E-09	1.27E-06	-0.59	-6.64	
35	214475_x_at	CAPN3	-7.68	1.24E-09	1.35E-06	-0.60	-6.62	15q15.1-q21.1
36	226640_at	LOC221955	-1.94	1.14E-08	7.08E-06	-0.62	-6.52	7p22.2
37	232424_at	PRDM16	9.69	1.70E-06	2.01E-04	1.16	6.52	1p36.23-p33
38	210150_s_at	LAMA5	-2.22	3.39E-09	2.79E-06	-0.59	-6.51	20q13.2-q13.3
39	221560_at	MARK4	-2.20	1.73E-09	1.65E-06	-0.57	-6.50	19q13.3
40	205366_s_at	HOXB6	16.00	1.82E-06	2.11E-04	1.15	6.49	17q21.3
41	244413_at	DCAL1	-3.48	2.53E-09	2.33E-06	-0.58	-6.46	12p13.2
42	208698_s_at	NONO	-1.72	4.57E-08	1.68E-05	-0.65	-6.46	Xq13.1
43	204612_at	PKIA	2.61	1.02E-06	1.39E-04	0.87	6.45	8q21.11
44	231775_at		-2.59	1.82E-08	9.47E-06	-0.61	-6.42	
45	224773_at	NAV1	-2.62	3.52E-09	2.80E-06	-0.57	-6.42	
46	229908_s_at	CAB56184	1.97	7.20E-07	1.11E-04	0.81	6.42	16p13.3
47	218892_at	PCDH16	-2.31	2.21E-08	1.08E-05	-0.61	-6.36	11p15.4
48	202315_s_at	BCR	-1.64	1.57E-08	8.74E-06	-0.59	-6.34	22q11.23
49	201288_at	ARHGDIB	-1.33	2.13E-07	4.89E-05	-0.68	-6.32	12p12.3
50	64408_s_at	MGC4809	-2.13	2.15E-08	1.08E-05	-0.60	-6.32	15q22.2
2.3	inv3 versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205382_s_at	DF	-6.46	4.97E-25	1.13E-20	-1.18	-13.29	19p13.3
2	202759_s_at	AKAP2	-3.39	7.20E-17	3.27E-13	-0.99	-10.68	9q31-q33
3	242621_at	FLJ32468	-1.53	1.64E-14	3.11E-11	-1.04	-10.66	7q22.1
4	228161_at	RAB32	-2.13	8.90E-18	9.02E-14	-0.92	-10.28	6q24.2
5	223534_s_at	RPS6KL1	-1.99	4.86E-13	4.80E-10	-1.00	-10.06	14q24.2
6	212953_x_at	CALR	-2.71	1.19E-17	9.02E-14	-0.89	-10.00	19p13.3-p13.2
7	210115_at	RPL39L	-7.93	2.28E-17	1.29E-13	-0.90	-9.98	3q27
8	212318_at	TRN-SR	-2.27	1.03E-13	1.30E-10	-0.96	-9.94	7q32.2
9	223703_at	CDA017	-2.69	2.02E-15	5.29E-12	-0.91	-9.87	10q23.1
10	200700_s_at	KDELR2	-2.42	9.75E-15	2.01E-11	-0.92	-9.81	7p22.2
11	214575_s_at	AZU1	-6.38	3.02E-16	9.80E-13	-0.87	-9.68	19p13.3
12	204921_at	GAS8	-2.97	1.54E-16	5.83E-13	-0.85	-9.55	16q24.3
13	203949_at	MPO	-3.93	1.75E-12	1.59E-09	-0.93	-9.49	17q23.1
14	231300_at	LOC90835	-2.91	4.34E-14	5.79E-11	-0.87	-9.39	16p11.2
15	231736_x_at	MGST1	-3.72	8.09E-12	5.10E-09	-0.92	-9.26	12p12.3-p12.1
16	226789_at		-2.38	9.71E-13	9.18E-10	-0.88	-9.16	

17	204301_at	KIAA0711	-8.64	2.10E-15	5.29E-12	-0.81	-9.12	8p23.2
18	205131_x_at	SCGF	-6.25	3.59E-15	8.16E-12	-0.79	-8.98	19q13.3
19	202760_s_at	AKAP2	-4.21	2.17E-13	2.59E-10	-0.83	-8.92	9q31-q33
20	224886_at	STUB1	-1.76	7.73E-12	5.01E-09	-0.86	-8.86	16p13.3
21	203948_s_at	MPO	-4.76	2.30E-12	1.86E-09	-0.84	-8.84	17q23.1
22	230044_at		-2.88	1.54E-11	8.30E-09	-0.86	-8.79	
23	204647_at	HOMER3	-4.13	2.16E-14	3.76E-11	-0.78	-8.75	19p13.11
24	224918_x_at	MGST1	-3.41	3.23E-10	9.26E-08	-0.91	-8.73	12p12.3-p12.1
25	210783_x_at	SCGF	-5.85	2.56E-14	4.15E-11	-0.77	-8.64	19q13.3
26	230480_at	HIWI2	-3.13	3.91E-14	5.55E-11	-0.77	-8.63	11q21
27	204548_at	STAR	-8.65	2.80E-14	4.23E-11	-0.77	-8.62	8p11.2
28	205248_at	C21orf5	-1.82	1.05E-11	5.93E-09	-0.82	-8.56	21q22.2
29	240672_at		-1.53	3.51E-13	3.79E-10	-0.78	-8.53	
30	232250_at	KIAA1257	-2.91	1.98E-11	9.58E-09	-0.82	-8.51	3q21.3
31	211048_s_at	ERP70	-2.42	2.32E-13	2.63E-10	-0.76	-8.47	7q35
32	201186_at	LRPAP1	-2.41	3.24E-12	2.37E-09	-0.79	-8.45	4p16.3
33	243917_at		-1.41	2.18E-12	1.83E-09	-0.78	-8.38	
34	224841_x_at		1.47	2.25E-08	2.47E-06	0.99	8.33	
35	239656_at		-2.19	2.57E-12	1.95E-09	-0.77	-8.33	
36	211709_s_at	SCGF	-3.42	1.61E-09	3.17E-07	-0.88	-8.32	19q13.3
37	214315_x_at	CALR	-1.94	1.15E-10	3.93E-08	-0.82	-8.32	19p13.3-p13.2
38	208795_s_at	MCM7	-2.13	1.34E-10	4.34E-08	-0.81	-8.24	7q21.3-q22.1
39	200654_at	P4HB	-2.24	1.12E-09	2.56E-07	-0.85	-8.20	17q25
40	226123_at	LOC286180	-3.50	1.83E-12	1.59E-09	-0.75	-8.19	8q12.1
41	202185_at	PLOD3	-1.87	1.21E-10	3.99E-08	-0.80	-8.18	7q22
42	203675_at	NUCB2	-2.33	6.81E-11	2.66E-08	-0.79	-8.14	11p15.1-p14
43	219588_s_at	FLJ20311	-2.28	6.05E-11	2.45E-08	-0.78	-8.13	7q36.3
44	226694_at	AKAP2	-3.97	1.65E-11	8.73E-09	-0.76	-8.10	9q31-q33
45	227929_at		-8.16	4.11E-13	4.24E-10	-0.72	-8.10	
46	206395_at	DGKG	-2.78	3.30E-10	9.36E-08	-0.80	-8.06	3q27-q28
47	228500_at	FLJ32891	-1.54	1.23E-08	1.54E-06	-0.90	-8.05	19q13.12
48	224741_x_at		1.45	3.81E-08	3.68E-06	0.95	8.03	
49	202290_at	PDAP1	-2.39	1.70E-10	5.29E-08	-0.79	-8.03	7q22.1
50	206440_at	LIN7A	-5.69	2.39E-12	1.87E-09	-0.72	-8.01	12q21
2.4	t(15;17) versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211990_at	HLA-DPA1	-10.44	2.24E-43	4.90E-39	-1.87	-21.20	6p21.3
2	204425_at	ARHGAP4	-16.94	1.02E-33	1.12E-29	-1.54	-17.17	Xq28
3	205771_s_at	AKAP7	-9.70	3.81E-33	2.78E-29	-1.46	-16.49	6q23
4	214450_at	CTSW	8.51	5.55E-13	4.01E-11	2.59	16.08	11q13.1
5	209732_at	CLECSF2	-30.16	2.08E-30	1.14E-26	-1.49	-16.03	12p13-p12
6	221004_s_at	ITM2C	5.38	3.20E-13	2.39E-11	2.23	15.51	2q37

7	38487_at	STAB1	9.09	1.49E-12	9.64E-11	2.57	15.45	3p21.31
8	212953_x_at	CALR	3.17	2.18E-13	1.71E-11	2.05	15.10	19p13.3-p13.2
9	201137_s_at	HLA-DPB1	-11.06	1.59E-28	4.96E-25	-1.32	-14.76	6p21.3
10	211474_s_at	SERPINB6	-4.44	7.00E-29	2.55E-25	-1.31	-14.75	6p25
11	201923_at	PRDX4	-6.23	6.52E-29	2.55E-25	-1.30	-14.73	Xp22.13
12	201719_s_at	EPB41L2	-12.00	1.13E-27	3.10E-24	-1.29	-14.36	6q23
13	200931_s_at	VCL	-3.67	3.72E-26	5.82E-23	-1.29	-14.32	10q22.1-q23
14	213587_s_at	LOC155066	-5.25	1.35E-27	3.29E-24	-1.27	-14.25	7q36.1
15	208306_x_at	HLA-DRB4	-7.12	2.28E-27	4.99E-24	-1.27	-14.25	6p21.3
16	227353_at	EVER2	-3.66	1.48E-22	1.01E-19	-1.34	-14.24	17q25.3
17	209312_x_at	HLA-DRB1	-6.66	1.03E-26	1.89E-23	-1.26	-14.15	6p21.3
18	209619_at	CD74	-4.60	4.12E-20	1.73E-17	-1.37	-14.09	5q32
19	217478_s_at	HLA-DMA	-5.51	3.00E-27	5.97E-24	-1.24	-14.00	6p21.3
20	236554_x_at	EVER2	-3.57	8.71E-24	1.00E-20	-1.26	-13.76	17q25.3
21	217848_s_at	PP	-3.40	2.67E-22	1.73E-19	-1.28	-13.71	10q11.1-q24
22	200654_at	P4HB	2.12	3.43E-15	4.12E-13	1.51	13.68	17q25
23	204362_at	SCAP2	-10.71	2.36E-26	3.98E-23	-1.20	-13.57	7p21-p15
24	203948_s_at	MPO	2.73	1.13E-17	2.44E-15	1.36	13.52	17q23.1
25	204661_at	CDW52	-19.63	3.20E-25	4.37E-22	-1.20	-13.34	1p36
26	225639_at	SCAP2	-9.61	1.19E-25	1.73E-22	-1.18	-13.31	7p21-p15
27	228113_at	STAT3	-3.82	5.05E-23	4.09E-20	-1.19	-13.12	17q21
28	204670_x_at	HLA-DRB5	-5.39	3.35E-21	1.75E-18	-1.21	-13.01	6p21.3
29	211991_s_at	HLA-DPA1	-16.57	2.51E-24	3.23E-21	-1.17	-13.00	6p21.3
30	34210_at	CDW52	-24.45	1.10E-23	1.20E-20	-1.15	-12.74	1p36
31	241742_at	PRAM-1	-7.25	7.57E-24	9.20E-21	-1.13	-12.65	19p13.2
32	201034_at	ADD3	-4.03	1.12E-20	5.12E-18	-1.16	-12.59	10q24.2-q24.3
33	227598_at	LOC113763	-3.70	2.75E-23	2.60E-20	-1.12	-12.52	7q35
34	223280_x_at	MS4A6A	-16.52	8.79E-23	6.20E-20	-1.14	-12.45	11q12.1
35	226077_at	FLJ31951	-5.11	2.85E-23	2.60E-20	-1.10	-12.42	5q33.3
36	203535_at	S100A9	-7.03	7.53E-23	5.49E-20	-1.11	-12.40	1q21
37	204563_at	SELL	-5.94	1.82E-23	1.90E-20	-1.09	-12.36	1q23-q25
38	209288_s_at	CDC42EP3	-7.09	2.69E-23	2.60E-20	-1.09	-12.34	2p21
39	232617_at	CTSS	-5.39	4.63E-23	3.89E-20	-1.10	-12.33	1q21
40	217716_s_at	SEC61A1	2.10	1.23E-11	6.32E-10	1.64	12.27	3q21.3
41	208982_at	PECAM1	-4.56	3.28E-23	2.87E-20	-1.08	-12.25	17q23
42	221865_at	DKFZp547P234	-2.93	1.25E-20	5.58E-18	-1.12	-12.21	9q33.1
43	209448_at	HTATIP2	-6.78	6.40E-23	4.83E-20	-1.08	-12.20	11p15.1
44	226885_at		-2.87	9.67E-22	5.57E-19	-1.10	-12.18	
45	224356_x_at	MS4A6A	-16.66	4.97E-22	2.94E-19	-1.12	-12.15	11q12.1
46	216899_s_at	SCAP2	-5.20	6.39E-23	4.83E-20	-1.07	-12.15	7p21-p15
47	201753_s_at	ADD3	-4.84	4.78E-22	2.90E-19	-1.08	-12.09	10q24.2-q24.3
48	204361_s_at	SCAP2	-7.62	2.78E-22	1.74E-19	-1.06	-11.98	7p21-p15

49	238022_at		4.86	1.21E-11	6.21E-10	1.55	11.98	
50	203299_s_at	AP1S2	-3.85	2.69E-22	1.73E-19	-1.06	-11.95	Xp22.31
2.5	t(821) versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	225615_at	LOC126917	-6.47	2.83E-26	8.92E-22	-1.20	-13.56	1p36.13
2	215087_at		-3.10	8.13E-22	1.28E-17	-1.04	-11.71	
3	221581_s_at	WBSCR5	-5.40	1.39E-21	1.46E-17	-1.03	-11.59	7q11.23
4	224764_at	ARHGAP10	-5.56	1.92E-21	1.51E-17	-1.02	-11.54	10
5	201425_at	ALDH2	-7.55	6.33E-21	3.99E-17	-1.01	-11.35	12q24.2
6	238077_at	MGC27385	-3.41	4.41E-20	1.74E-16	-1.02	-11.34	3p21.1
7	220974_x_at	BA108L7.2	-4.55	4.08E-20	1.74E-16	-1.01	-11.27	10q24.31
8	204494_s_at	DKFZP434H132	-3.00	2.40E-20	1.26E-16	-0.99	-11.14	15q22.33
9	226865_at		-5.33	9.25E-20	2.92E-16	-0.97	-10.92	
10	204495_s_at	DKFZP434H132	-2.98	6.35E-20	2.22E-16	-0.96	-10.91	15q22.33
11	209500_x_at	TNFSF13	-3.01	2.97E-18	7.82E-15	-0.95	-10.56	17p13.1
12	201944_at	HEXB	-2.37	2.13E-18	6.09E-15	-0.91	-10.31	5q13
13	227279_at	MGC15737	-2.42	1.63E-15	2.06E-12	-0.95	-10.19	Xq22.1
14	210314_x_at	TNFSF13	-3.48	1.19E-16	2.09E-13	-0.93	-10.19	17p13.1
15	200788_s_at	PEA15	-2.20	8.80E-15	6.77E-12	-0.96	-10.12	1q21.1
16	208890_s_at	PLXNB2	-3.44	9.94E-17	2.07E-13	-0.91	-10.06	22q13.33
17	208146_s_at	CPVL	-11.77	2.37E-17	5.74E-14	-0.89	-9.96	7p15-p14
18	227995_at		-6.95	6.87E-17	1.55E-13	-0.90	-9.85	
19	240572_s_at		-3.63	1.05E-16	2.07E-13	-0.88	-9.82	
20	213147_at	HOXA10	-7.74	1.17E-16	2.09E-13	-0.85	-9.62	7p15-p14
21	214651_s_at	HOXA9	-90.11	5.65E-16	8.10E-13	-0.90	-9.51	7p15-p14
22	217226_s_at	BA108L7.2	-2.91	3.90E-15	3.84E-12	-0.87	-9.49	10q24.31
23	206120_at	CD33	-4.19	2.12E-16	3.52E-13	-0.84	-9.48	19q13.3
24	227276_at	TEM7R	-2.62	2.32E-15	2.65E-12	-0.86	-9.47	10p12.1
25	203320_at	LNK	-2.28	6.01E-15	4.99E-12	-0.86	-9.38	12q24
26	225245_x_at	H2AFJ	-3.58	2.36E-15	2.65E-12	-0.84	-9.36	12p12
27	213150_at	HOXA10	-24.16	1.08E-15	1.49E-12	-0.86	-9.35	7p15-p14
28	207839_s_at	LOC51754	-2.83	1.26E-11	3.71E-09	-0.96	-9.34	9p13.1
29	200838_at	CTSB	-2.68	4.59E-15	4.26E-12	-0.85	-9.33	8p22
30	205639_at	AOAH	-3.88	1.02E-14	7.66E-12	-0.85	-9.33	7p14-p12
31	224049_at	KCNK17	-2.66	5.20E-16	8.10E-13	-0.82	-9.32	6p21.1
32	207075_at	CIAS1	-3.61	5.59E-16	8.10E-13	-0.82	-9.30	1q44
33	203017_s_at	SSX2IP	-2.91	2.24E-14	1.50E-11	-0.85	-9.21	
34	201887_at	IL13RA1	-2.98	5.03E-15	4.41E-12	-0.83	-9.19	Xq24
35	220066_at	CARD15	-5.86	1.34E-15	1.77E-12	-0.81	-9.17	16p12-q21
36	208091_s_at	DKFZP564K0822	-4.41	5.18E-15	4.41E-12	-0.81	-9.08	7p14.1
37	224393_s_at	CECR6	-8.27	4.33E-15	4.14E-12	-0.82	-9.05	
38	205419_at	EBI2	-4.20	2.95E-15	3.01E-12	-0.80	-9.05	13q32.2

39	212895_s_at	ABR	-2.64	3.93E-13	1.88E-10	-0.86	-9.04	17p13.3
40	209803_s_at	TSSC3	-5.16	2.42E-15	2.65E-12	-0.80	-9.04	11p15.5
41	238455_at		-3.51	2.44E-15	2.65E-12	-0.80	-9.03	
42	201850_at	CAPG	-4.57	2.96E-15	3.01E-12	-0.80	-9.03	2cen-q24
43	201105_at	LGALS1	-4.17	1.83E-14	1.31E-11	-0.82	-9.01	22q13.1
44	227853_at		-2.57	1.24E-11	3.69E-09	-0.91	-9.01	
45	201360_at	CST3	-3.55	6.33E-14	3.70E-11	-0.83	-8.99	20p11.21
46	242931_at		-2.79	3.90E-14	2.46E-11	-0.82	-8.96	
47	214835_s_at	SUCLG2	-3.26	1.29E-13	6.91E-11	-0.83	-8.94	3p14.2
48	204057_at	ICSBP1	-3.56	4.82E-15	4.34E-12	-0.79	-8.91	16q24.1
49	223132_s_at	TRIM8	-2.24	4.93E-14	3.05E-11	-0.81	-8.91	10q24.3
50	223398_at	MGC11115	-2.37	1.29E-13	6.91E-11	-0.82	-8.87	9q22.2
2.6	tMLL versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202746_at	ITM2A	-11.43	5.44E-24	1.38E-19	-1.15	-12.84	Xq13.3-Xq21.2
2	202747_s_at	ITM2A	-11.40	1.57E-22	1.98E-18	-1.09	-12.15	Xq13.3-Xq21.2
3	200953_s_at	CCND2	-3.77	6.25E-22	5.27E-18	-1.04	-11.75	12p13
4	225831_at	LOC148894	-3.55	4.79E-21	3.03E-17	-1.01	-11.43	1p36.11
5	225344_at	ERAP140	-3.84	1.11E-20	4.82E-17	-1.02	-11.38	6q22.33
6	226517_at	BCAT1	-8.89	3.57E-20	1.00E-16	-1.01	-11.22	12pter-q12
7	218966_at	MYO5C	-2.56	1.14E-20	4.82E-17	-0.99	-11.21	15q21
8	201830_s_at	NET1	-3.67	1.39E-20	5.00E-17	-0.99	-11.19	10p15
9	221235_s_at		-2.20	2.89E-20	9.15E-17	-0.98	-11.05	
10	200665_s_at	SPARC	-8.80	1.44E-19	3.65E-16	-0.96	-10.84	5q31.3-q32
11	200951_s_at	CCND2	-4.27	2.90E-19	6.67E-16	-0.94	-10.64	12p13
12	213737_x_at		2.20	2.63E-13	1.19E-10	1.15	10.54	
13	225653_at		-1.81	1.42E-18	2.76E-15	-0.93	-10.45	
14	201829_at	NET1	-2.42	1.18E-18	2.49E-15	-0.92	-10.39	10p15
15	214651_s_at	HOXA9	4.96	6.25E-13	2.51E-10	1.14	10.32	7p15-p14
16	224049_at	KCNK17	-2.99	5.30E-18	8.93E-15	-0.92	-10.25	6p21.1
17	214390_s_at	BCAT1	-7.69	5.12E-18	8.93E-15	-0.91	-10.22	12pter-q12
18	200952_s_at	CCND2	-2.66	6.09E-18	9.63E-15	-0.90	-10.15	12p13
19	206761_at	TACTILE	-14.52	6.58E-17	9.79E-14	-0.96	-10.07	3q13.13
20	227297_at		-11.16	1.76E-16	2.47E-13	-0.90	-9.76	
21	200829_x_at	ZNF207	-1.50	1.67E-15	1.76E-12	-0.90	-9.71	17q11.2
22	220104_at	ZAP	-2.31	3.89E-15	3.64E-12	-0.87	-9.49	7q34
23	241756_at		-3.07	8.30E-16	9.54E-13	-0.85	-9.48	
24	225285_at		-7.25	3.04E-16	4.05E-13	-0.83	-9.41	
25	242051_at		-2.81	9.79E-16	1.08E-12	-0.84	-9.38	
26	241133_at	TRB	-6.23	4.52E-16	5.72E-13	-0.83	-9.37	7q34
27	206009_at	ITGA9	-2.73	6.77E-15	5.70E-12	-0.85	-9.31	3p21.3

28	212667_at	SPARC	-4.73	6.67E-16	8.03E-13	-0.82	-9.29	5q31.3-q32
29	204082_at	PBX3	5.29	3.64E-10	5.17E-08	1.33	9.19	9q33-q34
30	231259_s_at	CCND2	-2.27	6.26E-15	5.46E-12	-0.82	-9.10	12p13
31	219686_at	HSA250839	-9.83	9.59E-15	7.38E-12	-0.86	-9.08	4p16.2
32	223126_s_at	C1orf21	-4.19	2.86E-15	2.78E-12	-0.81	-9.07	1q25
33	236513_at		-2.87	2.43E-15	2.46E-12	-0.80	-9.05	
34	226152_at	TTC7L1	-2.36	1.61E-13	7.74E-11	-0.85	-8.99	14q32.12
35	225532_at	LOC91768	-3.22	4.14E-15	3.74E-12	-0.80	-8.97	18q11.1
36	226580_at	BRMS1	-2.02	3.03E-14	2.02E-11	-0.81	-8.91	14q13.1
37	226473_at	LOC147136	-3.00	1.39E-14	1.00E-11	-0.80	-8.89	17q25.3
38	221760_at	MAN1A1	-5.47	1.36E-14	1.00E-11	-0.80	-8.83	6q22
39	235818_at		-6.84	7.71E-15	6.29E-12	-0.78	-8.83	
40	211137_s_at	ATP2C1	-1.90	9.64E-15	7.38E-12	-0.78	-8.78	3q21-q24
41	221581_s_at	WBSCR5	2.92	2.60E-10	3.98E-08	1.06	8.77	7q11.23
42	218825_at	ZNEU1	-4.74	1.82E-14	1.28E-11	-0.78	-8.73	9q34.3
43	240084_at		-1.75	1.04E-12	3.75E-10	-0.84	-8.73	
44	235753_at		4.76	5.06E-10	7.03E-08	1.10	8.69	
45	208116_s_at	MAN1A1	-3.99	2.27E-14	1.55E-11	-0.77	-8.68	6q22
46	201015_s_at	JUP	-5.04	2.31E-13	1.06E-10	-0.79	-8.61	17q21
47	200923_at	LGALS3BP	-5.57	9.28E-14	5.06E-11	-0.81	-8.61	17q25
48	221831_at	LOC148894	-2.53	7.35E-13	2.82E-10	-0.80	-8.57	1p36.11
49	218899_s_at	BAALC	-6.51	9.62E-14	5.07E-11	-0.79	-8.57	8q22.3
50	205624_at	CPA3	-13.99	1.36E-13	6.83E-11	-0.81	-8.55	3q21-q25

Table 3

3. All-Pairs (AP)

3.1 M4eo versus PTD

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	235753_at		-8.40	1.24E-10	4.49E-07	-2.15	-11.39	
2	206847_s_at	HOXA7	-5.18	2.73E-11	2.32E-07	-1.81	-10.98	7p15-p14
3	201497_x_at	MYH11	18.86	2.02E-10	6.27E-07	2.05	10.66	16p13.13-p13.12
4	213908_at		-7.48	4.93E-10	1.14E-06	-1.78	-10.15	
5	213147_at	HOXA10	-5.00	9.04E-11	4.25E-07	-1.60	-9.96	7p15-p14
6	235359_at		3.64	1.33E-11	1.95E-07	1.48	9.72	
7	214651_s_at	HOXA9	-17.28	3.10E-09	3.62E-06	-1.80	-9.54	7p15-p14
8	201496_x_at	MYH11	5.22	1.00E-10	4.25E-07	1.49	9.47	16p13.13-p13.12
9	200953_s_at	CCND2	2.28	1.53E-11	1.95E-07	1.40	9.35	12p13
10	209406_at	BAG2	-5.34	3.13E-09	3.62E-06	-1.62	-9.21	6p12.3-p11.2
11	200951_s_at	CCND2	3.03	6.00E-11	3.81E-07	1.33	8.89	12p13
12	213150_at	HOXA10	-7.80	1.12E-08	9.12E-06	-1.55	-8.67	7p15-p14
13	217963_s_at	NGFRAP1	-13.60	1.45E-08	1.02E-05	-1.52	-8.52	Xq22.1

14	202746_at	ITM2A	3.65	2.22E-10	6.27E-07	1.27	8.48	Xq13.3-Xq21.2
15	202747_s_at	ITM2A	3.99	2.69E-10	6.85E-07	1.26	8.40	Xq13.3-Xq21.2
16	227533_at		-2.80	1.75E-09	2.62E-06	-1.32	-8.40	
17	226352_at		-7.39	2.41E-08	1.32E-05	-1.51	-8.35	
18	205330_at	MN1	8.19	1.15E-08	9.12E-06	1.43	8.29	22q12.1
19	226944_at	HTRA3	-4.12	6.84E-09	5.79E-06	-1.35	-8.27	4p16.1
20	209365_s_at	ECM1	2.54	6.72E-10	1.31E-06	1.25	8.24	1q21
21	223385_at	CYP2S1	2.26	1.16E-09	1.84E-06	1.24	8.14	19q13.1
22	201005_at	CD9	6.33	2.35E-09	3.02E-06	1.26	8.11	12p13.3
23	205600_x_at	HOXB5	-2.96	3.92E-08	1.84E-05	-1.37	-7.92	17q21.3
24	218214_at	FLJ11773	1.96	6.32E-10	1.31E-06	1.16	7.87	12q13.13
25	205830_at	CLGN	-7.01	5.00E-08	2.27E-05	-1.38	-7.87	4q28.3-q31.1
26	220591_s_at	FLJ22843	2.52	1.54E-08	1.03E-05	1.27	7.82	Xp11.3
27	211926_s_at	MYH9	1.88	9.38E-10	1.59E-06	1.15	7.80	22q13.1
28	217849_s_at	CDC42BPB	4.70	8.99E-10	1.59E-06	1.15	7.79	14q32.3
29	224772_at	NAV1	2.53	4.15E-09	4.58E-06	1.19	7.77	
30	225055_at	DKFZp667M2411	-3.67	1.76E-08	1.08E-05	-1.24	-7.75	17q11.2
31	209905_at	HOXA9	-48.57	1.40E-07	4.33E-05	-1.56	-7.72	7p15-p14
32	243010_at	MSI2	-3.13	8.47E-08	3.12E-05	-1.37	-7.70	17q23.1
33	241985_at	FLJ37870	-7.23	7.12E-08	2.72E-05	-1.34	-7.69	5q13.3
34	227224_at	FLJ25604	-4.72	3.63E-08	1.77E-05	-1.25	-7.62	1q24.2
35	212358_at	CLIPR-59	14.29	9.72E-08	3.43E-05	1.48	7.61	19q13.12
36	208033_s_at	ATBF1	3.24	5.57E-09	5.06E-06	1.15	7.57	16q22.3-q23.1
37	225346_at	LOC80298	-2.05	1.51E-08	1.03E-05	-1.18	-7.54	12q24.1
38	209190_s_at	DIAPH1	1.99	1.89E-09	2.67E-06	1.11	7.54	5q31
39	34210_at	CDW52	3.20	2.37E-09	3.02E-06	1.11	7.49	1p36
40	210139_s_at	PMP22	5.29	1.35E-08	9.81E-06	1.16	7.48	17p12-p11.2
41	223044_at	SLC11A3	-9.10	1.27E-07	4.04E-05	-1.31	-7.46	2q32
42	241525_at	LOC200772	45.22	1.44E-07	4.36E-05	1.44	7.43	2q37.3
43	224998_at	CKLFSF4	-2.08	5.48E-08	2.40E-05	-1.21	-7.42	16q21
44	210150_s_at	LAMA5	2.45	4.44E-09	4.71E-06	1.10	7.40	20q13.2-q13.3
45	230896_at		-19.18	2.83E-07	6.17E-05	-1.47	-7.37	
46	208873_s_at	DP1	3.10	1.79E-08	1.08E-05	1.13	7.35	5q22-q23
47	222786_at	C4S-2	-3.35	1.76E-07	4.82E-05	-1.29	-7.32	7p22
48	200984_s_at	CD59	-4.41	2.01E-07	5.16E-05	-1.29	-7.29	11p13
49	201389_at	ITGA5	2.13	6.03E-08	2.54E-05	1.19	7.28	12q11-q13
50	218418_s_at	KIAA1518	-2.74	1.02E-07	3.49E-05	-1.21	-7.28	19p13.13

3.2 M4eo versus inv3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	4.74	1.72E-13	4.54E-09	2.41	14.22	17q23.1

2	203948_s_at	MPO	5.13	2.36E-12	2.08E-08	1.89	11.46	17q23.1
3	205382_s_at	DF	5.65	1.05E-12	1.38E-08	1.83	11.19	19p13.3
4	201497_x_at	MYH11	18.46	2.05E-10	7.07E-07	2.06	10.65	16p13.13-p13.12
5	224841_x_at		-1.69	2.14E-10	7.07E-07	-1.76	-10.33	
6	224741_x_at		-1.69	3.09E-10	9.08E-07	-1.76	-10.28	
7	209365_s_at	ECM1	3.28	3.37E-11	2.23E-07	1.54	9.53	1q21
8	210755_at	HGF	6.18	6.96E-10	1.84E-06	1.65	9.44	7q21.1
9	228497_at	FLIPT1	-3.11	8.82E-09	1.17E-05	-1.63	-9.19	1p13.1
10	205718_at	ITGB7	3.07	1.91E-10	7.07E-07	1.44	8.88	12q13.13
11	205131_x_at	SCGF	4.37	1.79E-10	7.07E-07	1.40	8.73	19q13.3
12	217963_s_at	NGFRAP1	-20.39	5.19E-07	1.67E-04	-1.88	-8.49	Xq22.1
13	201496_x_at	MYH11	3.64	1.43E-09	3.16E-06	1.40	8.45	16p13.13-p13.12
14	222862_s_at	AK5	40.65	3.10E-08	2.93E-05	1.61	8.14	1p31
15	236646_at	FLJ31166	3.02	9.63E-10	2.31E-06	1.30	8.12	12p13.31
16	226197_at		2.75	2.51E-09	4.46E-06	1.31	8.04	
17	203074_at	ANXA8	1.80	2.08E-09	4.22E-06	1.30	8.04	10q11.2
18	243244_at		3.90	2.53E-09	4.46E-06	1.29	7.95	
19	202605_at	GUSB	2.22	4.26E-08	3.47E-05	1.30	7.70	7q21.11
20	212358_at	CLIPR-59	15.49	8.58E-08	5.04E-05	1.46	7.63	19q13.12
21	201360_at	CST3	3.63	4.80E-09	7.94E-06	1.22	7.62	20p11.21
22	226697_at	LOC92689	2.52	6.69E-09	1.04E-05	1.22	7.58	4p14
23	201462_at	KIAA0193	-5.29	3.06E-07	1.13E-04	-1.37	-7.57	7p14.3-p14.1
24	241525_at	LOC200772	55.36	1.35E-07	6.48E-05	1.47	7.46	2q37.3
25	210783_x_at	SCGF	4.12	8.13E-09	1.13E-05	1.20	7.46	19q13.3
26	231736_x_at	MGST1	3.57	7.41E-09	1.09E-05	1.19	7.44	12p12.3-p12.1
27	207961_x_at	MYH11	15.00	1.40E-07	6.63E-05	1.43	7.42	16p13.13-p13.12
28	224441_s_at	MGC14793	-3.13	8.20E-08	5.04E-05	-1.24	-7.37	6q16.3
29	205076_s_at	CRA	4.21	4.89E-08	3.77E-05	1.24	7.34	1q12-q21
30	210997_at	HGF	17.75	1.55E-07	6.94E-05	1.38	7.34	7q21.1
31	209975_at	CYP2E1	3.46	4.33E-08	3.47E-05	1.22	7.30	10q24.3-qter
32	224918_x_at	MGST1	3.27	1.58E-08	1.90E-05	1.18	7.29	12p12.3-p12.1
33	201069_at	MMP2	2.83	1.26E-08	1.59E-05	1.17	7.28	16q13-q21
34	202828_s_at	MMP14	5.47	1.26E-07	6.34E-05	1.29	7.25	14q11-q12
35	211709_s_at	SCGF	3.22	3.48E-08	3.08E-05	1.18	7.24	19q13.3
36	202283_at	SERPINF1	4.68	3.61E-08	3.08E-05	1.18	7.18	17p13.1
37	200852_x_at	GNB2	2.10	2.31E-08	2.65E-05	1.15	7.16	7q22
38	201688_s_at	TPD52	-3.31	7.77E-07	2.23E-04	-1.30	-7.14	8q21
39	219308_s_at	AK5	5.75	2.20E-07	9.06E-05	1.32	7.14	1p31
40	239814_at		2.34	2.50E-08	2.75E-05	1.14	7.12	
41	200985_s_at	CD59	-6.95	2.61E-06	5.15E-04	-1.42	-7.09	11p13
42	242621_at	FLJ32468	1.47	2.87E-08	2.81E-05	1.14	7.08	7q22.1
43	202185_at	PLOD3	1.78	2.78E-08	2.81E-05	1.14	7.07	7q22
44	223136_at	AIG-1	-5.06	9.07E-07	2.45E-04	-1.28	-7.05	6q24.1

45	223091_x_at	GL004	-1.53	1.27E-07	6.34E-05	-1.17	-7.04 2q36.3
46	223354_x_at	GL004	-1.62	2.88E-07	1.09E-04	-1.21	-7.04 2q36.3
47	214797_s_at	PCTK3	-2.39	4.15E-07	1.44E-04	-1.22	-7.03 1q31-q32
48	214558_at	GPR12	1.53	4.99E-08	3.77E-05	1.14	7.01 13q12
49	229309_at		4.49	6.27E-08	4.25E-05	1.15	7.01
50	205859_at	LY86	3.30	2.78E-08	2.81E-05	1.12	7.01 6p24.3

3.3 M4eo versus t(15;17)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211990_at	HLA-DPA1	12.88	7.26E-18	1.92E-13	3.35	20.08	6p21.3
2	214450_at	CTSW	-8.03	6.77E-13	7.14E-10	-3.05	-15.96	11q13.1
3	38487_at	STAB1	-8.03	2.37E-12	1.95E-09	-3.01	-15.25	3p21.31
4	221004_s_at	ITM2C	-5.22	1.41E-13	3.01E-10	-2.58	-15.04	2q37
5	204661_at	CDW52	33.75	1.67E-13	3.15E-10	2.69	14.74	1p36
6	200654_at	P4HB	-2.30	1.92E-15	1.27E-11	-2.31	-14.63	17q25
7	203535_at	S100A9	9.01	7.53E-16	6.62E-12	2.24	14.32	1q21
8	217478_s_at	HLA-DMA	7.63	2.80E-14	8.72E-11	2.35	14.21	6p21.3
9	209732_at	CLECSF2	30.47	5.76E-13	6.61E-10	2.71	14.20	12p13-p12
10	34210_at	CDW52	43.85	7.27E-13	7.14E-10	2.58	13.90	1p36
11	238022_at		-8.74	2.99E-12	2.25E-09	-2.41	-13.63	
12	209619_at	CD74	5.65	3.24E-16	4.28E-12	2.06	13.52	5q32
13	201923_at	PRDX4	7.22	7.48E-14	1.79E-10	2.16	13.28	Xp22.13
14	205624_at	CPA3	-9.54	1.00E-11	6.01E-09	-2.41	-13.24	3q21-q25
15	204563_at	SELL	9.35	7.30E-13	7.14E-10	2.25	13.07	1q23-q25
16	200931_s_at	VCL	3.96	1.06E-14	5.62E-11	2.01	12.90	10q22.1-q23
17	231310_at		4.74	2.97E-14	8.72E-11	2.04	12.89	
18	209312_x_at	HLA-DRB1	8.89	3.15E-13	4.37E-10	2.06	12.62	6p21.3
19	208306_x_at	HLA-DRB4	9.65	5.23E-13	6.43E-10	2.08	12.60	6p21.3
20	238365_s_at		-10.74	1.01E-10	3.36E-08	-2.50	-12.45	
21	208891_at	DUSP6	7.70	2.11E-14	8.72E-11	1.93	12.44	12q22-q23
22	212953_x_at	CALR	-2.84	2.97E-14	8.72E-11	-1.91	-12.34	19p13.3-p13.2
23	204670_x_at	HLA-DRB5	6.79	3.94E-14	1.04E-10	1.91	12.25	6p21.3
24	205718_at	ITGB7	6.61	6.63E-13	7.14E-10	1.97	12.10	12q13.13
25	205453_at	HOXB2	11.16	1.03E-11	6.03E-09	2.13	11.95	17q21-q22
26	205663_at	PCBP3	-4.69	1.37E-11	7.52E-09	-2.01	-11.85	21q22.3
27	232617_at	CTSS	8.88	1.90E-11	9.29E-09	2.15	11.78	1q21
28	207375_s_at	IL15RA	4.80	1.48E-13	3.01E-10	1.84	11.77	10p15-p14
29	224583_at	COTL1	5.58	3.11E-13	4.37E-10	1.86	11.77	16q23.3
30	221059_s_at	CHST6	6.80	4.13E-12	2.80E-09	1.95	11.67	16q22
31	233072_at	KIAA1857	-7.47	2.04E-10	5.49E-08	-2.19	-11.60	9q34
32	229168_at	DKFZp434K0621	-6.73	3.74E-10	8.88E-08	-2.36	-11.59	5q35.3
33	208982_at	PECAM1	4.84	2.17E-12	1.85E-09	1.88	11.55	17q23

34 224839_s_at	GPT2	-9.02	4.23E-11	1.75E-08	-1.95	-11.41	16q12.1
35 202803_s_at	ITGB2	5.43	5.36E-13	6.43E-10	1.72	11.07	21q22.3
36 223280_x_at	MS4A6A	24.98	9.94E-11	3.36E-08	2.11	11.04	11q12.1
37 201496_x_at	MYH11	10.61	1.13E-11	6.47E-09	1.81	10.98	16p13.13-p13.12
38 211991_s_at	HLA-DPA1	25.17	9.82E-11	3.36E-08	2.05	10.97	6p21.3
39 204150_at	STAB1	-9.71	1.08E-09	2.11E-07	-2.26	-10.94	3p21.31
40 208689_s_at	RPN2	-1.75	1.91E-13	3.36E-10	-1.66	-10.90	20q12-q13.1
41 220798_x_at	FLJ11535	-3.81	7.69E-11	2.82E-08	-1.84	-10.89	19p13.3
42 201497_x_at	MYH11	28.44	1.48E-10	4.48E-08	2.16	10.88	16p13.13-p13.12
43 202917_s_at	S100A8	3.19	3.79E-13	5.01E-10	1.66	10.85	1q21
44 241742_at	PRAM-1	11.60	1.23E-10	3.81E-08	1.97	10.76	19p13.2
45 228046_at	LOC152485	3.03	5.49E-12	3.54E-09	1.72	10.76	4q31.1
46 226878_at		4.19	1.90E-11	9.29E-09	1.77	10.75	
47 238604_at		3.63	2.30E-13	3.79E-10	1.62	10.71	
48 213779_at	LOC129080	-6.64	9.66E-10	1.96E-07	-2.04	-10.68	22q12.1
49 224356_x_at	MS4A6A	25.23	2.22E-10	5.74E-08	2.06	10.62	11q12.1
50 217897_at	FXYD6	3.03	3.34E-11	1.44E-08	1.77	10.62	11q23.3

3.4 M4eo versus t(821)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	207075_at	CIAS1	6.60	1.43E-12	1.58E-08	2.19	12.64	1q44
2	208890_s_at	PLXNB2	5.22	2.59E-13	7.61E-09	1.97	12.16	22q13.33
3	205453_at	HOXB2	12.65	7.66E-12	3.63E-08	2.15	12.07	17q21-q22
4	205419_at	EBI2	7.98	2.83E-12	2.35E-08	2.05	12.03	13q32.2
5	205718_at	ITGB7	6.53	4.59E-13	7.61E-09	1.89	11.75	12q13.13
6	224764_at	ARHGAP10	8.90	1.13E-11	4.17E-08	2.01	11.58	10
7	218795_at	ACP6	-4.56	4.74E-11	1.12E-07	-1.87	-11.10	1q21
8	201497_x_at	MYH11	26.30	1.55E-10	2.09E-07	2.14	10.85	16p13.13-p13.12
9	201496_x_at	MYH11	9.04	1.66E-11	5.52E-08	1.78	10.74	16p13.13-p13.12
10	200665_s_at	SPARC	4.57	5.30E-12	2.93E-08	1.71	10.65	5q31.3-q32
11	224049_at	KCNK17	4.59	1.14E-10	1.80E-07	1.91	10.65	6p21.1
12	224724_at	SULF2	27.22	4.07E-10	3.97E-07	1.99	10.29	20q12-13.2
13	218236_s_at	PRKCN	4.94	4.24E-12	2.81E-08	1.60	10.20	2p21
14	201425_at	ALDH2	7.88	2.04E-10	2.42E-07	1.71	9.98	12q24.2
15	203320_at	LNK	3.26	9.11E-11	1.71E-07	1.62	9.83	12q24
16	201944_at	HEXB	2.27	3.74E-11	9.55E-08	1.57	9.80	5q13
17	201360_at	CST3	5.61	9.57E-11	1.71E-07	1.59	9.72	20p11.21
18	209365_s_at	ECM1	3.24	2.77E-11	7.66E-08	1.52	9.61	1q21
19	201887_at	IL13RA1	4.89	3.33E-10	3.57E-07	1.62	9.59	Xq24
20	220974_x_at	BA108L7.2	5.51	2.19E-10	2.51E-07	1.57	9.52	10q24.31
21	201596_x_at	KRT18	7.84	1.81E-10	2.24E-07	1.56	9.52	12q13

22 221841_s_at		4.33	2.08E-11	6.27E-08	1.48	9.48	
23 238604_at		3.14	1.08E-11	4.17E-08	1.45	9.41	
24 202670_at	MAP2K1	3.54	5.66E-10	5.22E-07	1.58	9.36	15q22.1-q22.33
25 210314_x_at	TNFSF13	4.72	3.31E-10	3.57E-07	1.52	9.25	17p13.1
26 209500_x_at	TNFSF13	3.94	5.43E-10	5.15E-07	1.54	9.24	17p13.1
27 235359_at		2.92	1.82E-10	2.24E-07	1.46	9.12	
28 223249_at	CLDN12	3.41	1.57E-10	2.09E-07	1.43	9.00	7q21
29 201739_at	SGK	4.50	5.38E-11	1.19E-07	1.39	8.97	6q23
30 229309_at		11.01	3.92E-09	2.32E-06	1.64	8.96	
31 206940_s_at	POU4F1	-40.05	7.47E-08	1.80E-05	-2.03	-8.95	13q21.1-q22
32 218217_at	RISC	3.30	1.43E-10	2.06E-07	1.41	8.94	17q23.1
33 208683_at	CAPN2	3.27	9.79E-11	1.71E-07	1.38	8.88	1q41-q42
34 226818_at	LOC219972	10.92	2.55E-09	1.77E-06	1.53	8.85	11q12.1
35 240572_s_at		3.25	1.23E-10	1.86E-07	1.37	8.80	
36 212459_x_at	SUCLG2	3.68	8.62E-11	1.71E-07	1.35	8.76	3p14.2
37 229383_at		4.93	3.73E-09	2.27E-06	1.51	8.71	
38 205859_at	LY86	3.62	1.25E-09	1.04E-06	1.42	8.67	6p24.3
39 225602_at	C9orf19	2.80	1.09E-10	1.80E-07	1.34	8.67	9p13-p12
40 211341_at	POU4F1	-165.76	1.28E-07	2.73E-05	-2.00	-8.63	13q21.1-q22
41 203329_at	PTPRM	6.43	4.01E-09	2.33E-06	1.48	8.61	18p11.2
42 205330_at	MN1	9.71	9.34E-09	4.25E-06	1.60	8.60	22q12.1
43 204057_at	ICSBP1	4.44	4.46E-09	2.40E-06	1.47	8.57	16q24.1
44 236738_at		6.32	1.86E-09	1.40E-06	1.39	8.50	
45 211084_x_at	PRKCN	4.65	3.64E-10	3.67E-07	1.31	8.41	2p21
46 217849_s_at	CDC42BPB	4.67	3.44E-10	3.57E-07	1.30	8.39	14q32.3
47 208033_s_at	ATBF1	3.91	1.05E-09	9.16E-07	1.31	8.30	16q22.3-q23.1
48 205076_s_at	CRA	5.74	1.33E-08	5.44E-06	1.47	8.27	1q12-q21
49 228827_at		-103.82	2.39E-07	4.54E-05	-1.91	-8.25	
50 226841_at	LOC219972	12.37	1.88E-08	6.92E-06	1.51	8.24	11q12.1

3.5 M4eo versus tMLL

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213737_x_at		-3.81	2.63E-16	7.45E-12	-2.33	-15.21	
2	200665_s_at	SPARC	16.92	2.60E-13	1.47E-09	2.28	13.71	5q31.3-q32
3	214651_s_at	HOXA9	-24.73	4.60E-14	3.26E-10	-2.26	-13.54	7p15-p14
4	200953_s_at	CCND2	4.36	1.06E-15	1.50E-11	1.96	13.49	12p13
5	202746_at	ITM2A	15.99	1.64E-12	4.65E-09	2.15	12.76	Xq13.3-Xq21.2
6	202747_s_at	ITM2A	16.03	3.21E-12	8.28E-09	2.02	12.22	Xq13.3-Xq21.2
7	200951_s_at	CCND2	5.31	4.09E-13	1.66E-09	1.80	11.91	12p13
8	231310_at		4.76	7.45E-15	7.04E-11	1.67	11.82	
9	202551_s_at	CRIM1	4.27	3.61E-13	1.66E-09	1.61	11.06	2p21

10 227567_at		-5.39	7.34E-13	2.60E-09	-1.62	-10.92	
11 201497_x_at	MYH11	26.26	1.56E-10	1.30E-07	2.13	10.85	16p13.13-p13.12
12 205453_at	HOXB2	7.94	5.98E-12	1.30E-08	1.65	10.82	17q21-q22
13 224049_at	KCNK17	4.81	8.48E-11	8.90E-08	1.85	10.77	6p21.1
14 235753_at		-13.72	2.38E-11	3.96E-08	-1.85	-10.59	
15 201496_x_at	MYH11	6.89	5.88E-11	7.25E-08	1.72	10.56	16p13.13-p13.12
16 212667_at	SPARC	8.11	5.29E-11	6.97E-08	1.64	10.33	5q31.3-q32
17 206847_s_at	HOXA7	-6.82	1.92E-11	3.41E-08	-1.61	-10.23	7p15-p14
18 229215_at	ASCL2	-10.76	3.29E-11	4.91E-08	-1.63	-10.12	11p15.5
19 209905_at	HOXA9	-81.11	8.12E-11	8.85E-08	-1.80	-10.06	7p15-p14
20 202931_x_at	BIN1	3.10	1.12E-12	3.53E-09	1.42	10.04	2q14
21 213147_at	HOXA10	-6.16	1.50E-11	2.84E-08	-1.51	-9.96	7p15-p14
22 201830_s_at	NET1	4.25	1.11E-10	1.12E-07	1.50	9.70	10p15
23 226517_at	BCAT1	10.34	5.88E-10	3.33E-07	1.61	9.63	12pter-q12
24 213150_at	HOXA10	-10.83	1.56E-10	1.30E-07	-1.57	-9.57	7p15-p14
25 213908_at		-15.52	3.82E-10	2.40E-07	-1.60	-9.31	
26 204082_at	PBX3	-5.53	3.07E-10	2.12E-07	-1.54	-9.31	9q33-q34
27 228058_at	LOC124220	6.00	6.45E-12	1.31E-08	1.29	9.24	16p13.3
28 203949_at	MPO	3.13	3.59E-11	5.08E-08	1.33	9.17	17q23.1
29 242738_s_at		2.48	2.90E-10	2.06E-07	1.40	9.16	
30 225831_at	LOC148894	3.66	1.72E-10	1.37E-07	1.37	9.16	1p36.11
31 224952_at	DKFZP564D166	-3.41	4.56E-12	1.08E-08	-1.27	-9.14	17q23.3
32 202370_s_at	CBFB	-3.09	2.04E-10	1.49E-07	-1.41	-9.12	16q22.1
33 205330_at	MN1	17.21	4.19E-09	1.40E-06	1.73	9.08	22q12.1
34 223471_at	RAB3IP	-3.52	7.55E-11	8.56E-08	-1.32	-9.03	
35 223385_at	CYP2S1	2.42	3.14E-10	2.12E-07	1.36	9.02	19q13.1
36 210139_s_at	PMP22	9.18	3.17E-09	1.18E-06	1.54	8.97	17p12-p11.2
37 201029_s_at	CD99	1.88	3.17E-11	4.91E-08	1.26	8.91	Xp22.32
38 226137_at		3.72	1.92E-09	8.26E-07	1.43	8.86	
39 218966_at	MYO5C	3.05	2.27E-09	9.48E-07	1.41	8.76	15q21
40 224772_at	NAV1	2.83	8.86E-10	4.74E-07	1.34	8.76	
41 203733_at	MYLE	-3.28	1.29E-10	1.26E-07	-1.27	-8.75	16p13.2
42 203329_at	PTPRM	6.00	6.69E-09	1.95E-06	1.52	8.68	18p11.2
43 211012_s_at	PML	2.73	5.41E-11	6.97E-08	1.22	8.68	15q22
44 202265_at	BMI1	-3.09	3.65E-10	2.40E-07	-1.30	-8.66	10p11.23
45 214452_at	BCAT1	4.20	1.00E-09	4.89E-07	1.31	8.63	12pter-q12
46 242686_at		2.41	2.36E-09	9.69E-07	1.36	8.62	
47 212771_at	LOC221061	5.21	1.07E-08	2.68E-06	1.58	8.58	10p13
48 200602_at	APP	6.12	1.47E-10	1.30E-07	1.22	8.57	21q21.3
49 228496_s_at	CRIM1	2.79	1.54E-10	1.30E-07	1.21	8.52	2p21
50 210006_at	DKFZP564O243	-2.19	7.82E-10	4.34E-07	-1.29	-8.49	3p21.1

3.6 PTD versus inv3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	229116_at		8.14	5.54E-07	1.82E-03	1.33	6.95	
2	235753_at		2.97	5.69E-08	1.40E-03	1.13	6.87	
3	205600_x_at	HOXB5	2.38	3.90E-07	1.82E-03	1.14	6.60	17q21.3
4	214643_x_at	BIN1	-2.90	2.16E-06	2.51E-03	-1.15	-6.43	2q14
5	205382_s_at	DF	4.56	1.23E-06	2.02E-03	1.10	6.28	19p13.3
6	209679_s_at	LOC57228	-3.63	6.67E-06	5.48E-03	-1.19	-6.27	12q13.12
7	228161_at	RAB32	1.67	5.28E-07	1.82E-03	1.05	6.26	6q24.2
8	226697_at	LOC92689	2.24	4.73E-07	1.82E-03	1.04	6.25	4p14
9	211084_x_at	PRKCN	-2.18	8.67E-07	2.02E-03	-1.05	-6.24	2p21
10	213110_s_at	COL4A5	18.16	3.89E-06	3.68E-03	1.26	6.17	Xq22
11	224918_x_at	MGST1	3.11	5.28E-07	1.82E-03	1.01	6.13	12p12.3-p12.1
12	231736_x_at	MGST1	3.26	5.91E-07	1.82E-03	1.01	6.11	12p12.3-p12.1
13	215016_x_at	BPAG1	3.91	5.81E-07	1.82E-03	1.00	6.10	6p12-p11
14	226789_at		2.44	1.21E-06	2.02E-03	1.03	6.08	
15	233893_s_at	KIAA1530	1.52	7.27E-07	1.99E-03	1.00	6.04	4p16.3
16	232250_at	KIAA1257	3.80	2.55E-06	2.51E-03	1.05	5.99	3q21.3
17	218552_at	FLJ10948	2.00	9.91E-07	2.02E-03	0.99	5.98	1p32.3
18	226197_at		2.36	1.63E-06	2.34E-03	1.00	5.94	
19	206847_s_at	HOXA7	2.13	1.13E-06	2.02E-03	0.97	5.88	7p15-p14
20	218709_s_at	C20orf9	1.60	1.18E-06	2.02E-03	0.97	5.87	
21	236892_s_at		6.01	8.37E-06	6.10E-03	1.11	5.78	
22	212254_s_at	BPAG1	3.37	1.51E-06	2.32E-03	0.95	5.78	6p12-p11
23	209406_at	BAG2	2.41	1.99E-06	2.51E-03	0.95	5.75	6p12.3-p11.2
24	225464_at	C14orf31	2.28	1.71E-06	2.34E-03	0.94	5.74	14q21.3
25	228252_at	PIF1	2.29	2.21E-06	2.51E-03	0.95	5.73	15q22.1
26	205767_at	EREG	11.02	9.66E-06	6.10E-03	1.10	5.72	4q21.1
27	205830_at	CLGN	3.48	2.41E-06	2.51E-03	0.94	5.68	4q28.3-q31.1
28	205514_at	FLJ11191	-2.72	1.42E-05	7.13E-03	-1.03	-5.67	19q13.41
29	240151_at		2.28	2.31E-06	2.51E-03	0.93	5.66	
30	205330_at	MN1	-7.45	4.85E-05	1.09E-02	-1.23	-5.65	22q12.1
31	214651_s_at	HOXA9	3.07	2.52E-06	2.51E-03	0.93	5.63	7p15-p14
32	201829_at	NET1	-2.38	2.74E-05	8.76E-03	-1.03	-5.52	10p15
33	204301_at	KIAA0711	4.79	1.26E-05	7.12E-03	0.99	5.48	8p23.2
34	242621_at	FLJ32468	1.54	9.56E-06	6.10E-03	0.95	5.45	7q22.1
35	230051_at		-2.32	2.38E-05	8.38E-03	-0.98	-5.43	
36	244297_at	FLJ35740	3.45	1.56E-05	7.13E-03	0.98	5.40	9p12
37	202232_s_at	GA17	-1.60	6.52E-06	5.48E-03	-0.90	-5.39	11p13
38	213147_at	HOXA10	2.19	5.23E-06	4.77E-03	0.89	5.39	7p15-p14
39	209905_at	HOXA9	4.12	8.60E-06	6.10E-03	0.91	5.36	7p15-p14
40	205601_s_at	HOXB5	2.42	5.97E-06	5.25E-03	0.88	5.36	17q21.3
41	232424_at	PRDM16	5.47	8.84E-06	6.10E-03	0.90	5.35	1p36.23-p33
42	213150_at	HOXA10	2.61	7.01E-06	5.57E-03	0.88	5.33	7p15-p14
43	239791_at		5.52	1.96E-05	7.90E-03	0.98	5.33	

44	214684_at	MEF2A	-1.80	1.23E-05	7.12E-03	-0.90	-5.32	15q26
45	202600_s_at	NRIP1	-3.90	8.68E-05	1.23E-02	-1.13	-5.31	21q11.2
46	203462_x_at	EIF3S9	1.73	7.66E-06	5.89E-03	0.87	5.29	7p22.3
47	223463_at	RAB23	2.75	1.33E-05	7.13E-03	0.91	5.29	6p11.2-p12.3
48	216035_x_at	TCF7L2	-2.37	4.09E-05	1.08E-02	-0.97	-5.28	10q25.3
49	206725_x_at	BMP1	1.74	1.60E-05	7.13E-03	0.91	5.26	8p21
50	222755_s_at	KIAA1416	1.70	1.04E-05	6.22E-03	0.88	5.25	8q12.1

3.7 PTD versus t(15;17)

#	affy Id	HUGO name	fc	p	q	stn	t	Map Location
1	214450_at	CTSW	-8.49	5.28E-14	2.10E-10	-2.60	-15.24	11q13.1
2	221004_s_at	ITM2C	-5.89	3.54E-15	3.51E-11	-2.19	-13.79	2q37
3	38487_at	STAB1	-6.66	2.22E-13	7.33E-10	-2.30	-13.71	3p21.31
4	212953_x_at	CALR	-3.25	6.25E-15	4.13E-11	-2.14	-13.47	19p13.3-p13.2
5	214789_x_at	SRP46	4.03	1.12E-15	2.22E-11	2.07	13.30	11q22
6	213147_at	HOXA10	19.18	1.60E-11	1.80E-08	2.44	12.72	7p15-p14
7	200654_at	P4HB	-2.49	1.62E-14	8.06E-11	-1.82	-11.76	17q25
8	206847_s_at	HOXA7	6.88	9.35E-12	1.33E-08	2.00	11.70	7p15-p14
9	235753_at		10.05	9.19E-11	6.52E-08	2.29	11.69	
10	233072_at	KIAA1857	-7.46	8.29E-11	6.19E-08	-1.96	-11.21	9q34
11	212509_s_at		-6.36	2.03E-10	1.30E-07	-2.05	-11.21	
12	200953_s_at	CCND2	-3.41	5.36E-11	4.68E-08	-1.91	-11.12	12p13
13	217716_s_at	SEC61A1	-2.20	7.55E-13	2.14E-09	-1.72	-10.96	3q21.3
14	208852_s_at	CANX	-2.75	3.10E-12	6.16E-09	-1.70	-10.72	5q35
15	203948_s_at	MPO	-3.32	1.03E-12	2.56E-09	-1.66	-10.64	17q23.1
16	210788_s_at	retSDR4	-2.44	1.63E-11	1.80E-08	-1.70	-10.51	14q22.3
17	AFFX-HSAC07/X00351_M_at - HG-U133B	ACTB	-2.29	1.37E-12	3.03E-09	-1.60	-10.33	7p15-p12
18	217225_x_at	LOC283820	-2.14	4.38E-12	7.25E-09	-1.63	-10.32	16p13.13
19	214651_s_at	HOXA9	165.30	1.46E-09	4.78E-07	2.15	10.16	7p15-p14
20	204150_at	STAB1	-7.16	9.18E-10	3.88E-07	-1.80	-10.10	3p21.31
21	228760_at		6.67	8.42E-11	6.19E-08	1.65	10.00	
22	213587_s_at	LOC155066	5.20	9.89E-10	3.89E-07	1.83	9.97	7q36.1
23	229168_at	DKFZp434K0621	-4.14	9.82E-10	3.89E-07	-1.73	-9.87	5q35.3
24	213106_at		4.55	5.67E-11	4.69E-08	1.60	9.86	
25	205771_s_at	AKAP7	12.68	1.65E-09	5.13E-07	1.85	9.83	6q23
26	213150_at	HOXA10	31.06	2.47E-09	6.53E-07	1.96	9.81	7p15-p14
27	205382_s_at	DF	-2.68	3.99E-12	7.20E-09	-1.51	-9.80	19p13.3
28	AFFX-HSAC07/X00351_M_at - HG-U133A	ACTB	-2.16	5.86E-12	8.94E-09	-1.49	-9.62	7p15-p12
29	205663_at	PCBP3	-3.00	2.34E-10	1.36E-07	-1.57	-9.57	21q22.3
30	211934_x_at	G2AN	-3.22	1.80E-10	1.19E-07	-1.56	-9.57	11q12.2
31	209215_at	TETRAN	-2.79	4.57E-11	4.32E-08	-1.51	-9.53	4p16.3
32	241383_at		-3.94	5.71E-09	1.27E-06	-1.80	-9.53	

33	200951_s_at	CCND2	-4.27	9.07E-10	3.88E-07	-1.62	-9.53	12p13
34	201596_x_at	KRT18	-6.62	5.70E-10	2.83E-07	-1.59	-9.49	12q13
35	204425_at	ARHGAP4	14.20	3.21E-09	8.18E-07	1.79	9.49	Xq28
36	201004_at	SSR4	-2.23	2.24E-10	1.36E-07	-1.54	-9.45	Xq28
37	226885_at		3.33	5.69E-10	2.83E-07	1.58	9.42	
38	238365_s_at		-3.90	7.10E-10	3.36E-07	-1.58	-9.41	
39	211709_s_at	SCGF	-3.62	2.22E-11	2.32E-08	-1.46	-9.37	19q13.3
40	200047_s_at - HG-U133A	YY1	1.88	1.47E-11	1.80E-08	1.44	9.33	14q
41	208675_s_at	DDOST	-2.23	1.48E-11	1.80E-08	-1.44	-9.33	1p36.1
42	228046_at	LOC152485	4.74	3.68E-09	9.03E-07	1.71	9.29	4q31.1
43	200640_at	YWHAZ	-1.82	2.97E-11	2.94E-08	-1.44	-9.26	8q23.1
44	209344_at	TPM4	-8.94	1.35E-08	2.57E-06	-1.80	-9.20	19p13.1
45	208689_s_at	RPN2	-1.93	5.43E-11	4.68E-08	-1.43	-9.15	20q12-q13.1
46	227353_at	EVER2	3.54	4.02E-10	2.22E-07	1.45	8.99	17q25.3
47	227326_at		-3.53	2.12E-09	5.95E-07	-1.51	-8.98	
48	209021_x_at	KIAA0652	-3.43	2.28E-10	1.36E-07	-1.42	-8.96	11p11.12
49	229564_at	dJ222E13.1	4.36	9.98E-10	3.89E-07	1.48	8.95	22q13
50	219837_s_at	C17	-11.98	2.18E-08	3.38E-06	-1.70	-8.85	4p16-p15

3.8 PTD versus t(821)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213147_at	HOXA10	12.09	1.79E-11	4.68E-07	2.20	12.11	7p15-p14
2	206847_s_at	HOXA7	5.90	3.18E-11	4.68E-07	2.10	11.64	7p15-p14
3	235753_at		8.83	1.07E-10	1.04E-06	2.19	11.46	
4	213908_at		7.63	5.10E-10	3.75E-06	1.86	10.22	
5	214651_s_at	HOXA9	141.82	1.49E-09	8.74E-06	2.13	10.15	7p15-p14
6	213150_at	HOXA10	37.05	2.25E-09	1.10E-05	1.98	9.86	7p15-p14
7	201281_at	ADRM1	-2.10	4.47E-09	1.88E-05	-1.54	-8.94	20q13.33
8	217963_s_at	NGFRAP1	19.39	1.15E-08	2.60E-05	1.68	8.83	Xq22.1
9	206940_s_at	POU4F1	-17.73	1.02E-07	1.20E-04	-1.77	-8.59	13q21.1-q22
10	211341_at	POU4F1	-28.93	1.74E-07	1.74E-04	-1.75	-8.33	13q21.1-q22
11	228827_at		-79.09	2.50E-07	2.04E-04	-1.90	-8.22	
12	209905_at	HOXA9	364.38	1.07E-07	1.21E-04	1.67	7.87	7p15-p14
13	211728_s_at	HYAL3	-3.88	8.31E-08	1.02E-04	-1.35	-7.73	3p21.3
14	205600_x_at	HOXB5	2.98	3.24E-08	5.02E-05	1.32	7.71	17q21.3
15	243806_at		4.67	6.31E-08	8.43E-05	1.36	7.67	
16	205529_s_at	CBFA2T1	-12.57	6.09E-07	3.44E-04	-1.65	-7.65	8q22
17	217520_x_at	LOC283683	5.38	1.61E-07	1.69E-04	1.54	7.64	15q11.2
18	226206_at	FLJ32205	2.71	2.98E-08	4.87E-05	1.27	7.57	7p22.3
19	243010_at	MSI2	3.10	8.08E-08	1.02E-04	1.33	7.54	17q23.1
20	AFFX-HSAC07/X00351_M_at - HG-U133B	ACTB	-1.94	9.85E-09	2.60E-05	-1.19	-7.46	7p15-p12
21	AFFX-	ACTB	-1.94	7.31E-09	2.39E-05	-1.18	-7.45	7p15-p12

	HSAC07/X00351_M_at - HG-U133A							
22	210150_s_at	LAMA5	-4.43	4.65E-07	2.97E-04	-1.41	-7.42	20q13.2-q13.3
23	AFFX-HSAC07/X00351_3_at - HG-U133A	ACTB	-1.28	1.15E-08	2.60E-05	-1.19	-7.41	7p15-p12
24	218453_s_at	C6orf35	1.62	7.91E-09	2.39E-05	1.17	7.39	6q25.3
25	227853_at		2.48	8.14E-09	2.39E-05	1.16	7.36	
26	224998_at	CKLFSF4	2.27	1.85E-08	3.39E-05	1.18	7.34	16q21
27	219598_s_at	PTD013	1.80	1.31E-08	2.76E-05	1.17	7.34	6q13-q22.33
28	205453_at	HOXB2	18.65	2.99E-07	2.20E-04	1.47	7.34	17q21-q22
29	207839_s_at	LOC51754	3.80	4.98E-08	7.32E-05	1.22	7.31	9p13.1
30	201288_at	ARHGDIB	-1.50	1.72E-08	3.37E-05	-1.16	-7.25	12p12.3
31	235521_at	HOXA3	11.11	4.78E-07	2.99E-04	1.42	7.11	7p15-p14
32	205601_s_at	HOXB5	3.02	2.30E-07	1.99E-04	1.25	7.09	17q21.3
33	210633_x_at	KRT10	2.05	2.61E-08	4.51E-05	1.10	6.98	17q21-q23
34	233955_x_at	HSPC195	3.02	2.47E-07	2.04E-04	1.21	6.97	5q31.3
35	228058_at	LOC124220	-2.78	3.08E-07	2.21E-04	-1.17	-6.88	16p13.3
36	202315_s_at	BCR	-1.95	1.88E-07	1.74E-04	-1.14	-6.87	22q11.23
37	220558_x_at	PHEMX	2.09	5.85E-08	8.19E-05	1.09	6.82	11p15.5
38	205528_s_at	CBFA2T1	-33.41	2.96E-06	8.37E-04	-1.54	-6.82	8q22
39	205366_s_at	HOXB6	35.11	1.11E-06	5.01E-04	1.40	6.75	17q21.3
40	218236_s_at	PRKCN	3.85	1.59E-07	1.69E-04	1.10	6.74	2p21
41	233467_s_at	PHEMX	2.23	1.90E-07	1.74E-04	1.09	6.68	11p15.5
42	239707_at	FLJ25217	-4.23	1.60E-06	6.01E-04	-1.21	-6.64	17p11.2
43	226235_at	MGC17515	2.37	2.92E-07	2.20E-04	1.07	6.52	18p11.23
44	208146_s_at	CPVL	11.95	1.58E-06	6.01E-04	1.24	6.50	7p15-p14
45	228359_at	KIAA1959	-2.35	8.71E-07	4.44E-04	-1.10	-6.46	11q24.1
46	228345_at		2.77	2.88E-07	2.20E-04	1.05	6.46	
47	202732_at	PKIG	2.08	2.72E-07	2.16E-04	1.04	6.45	20q12-q13.1
48	232424_at	PRDM16	9.40	1.72E-06	6.33E-04	1.21	6.44	1p36.23-p33
49	225765_at	KPNB2	1.97	2.15E-07	1.92E-04	1.02	6.40	5q13.1
50	203859_s_at	PALM	-3.60	2.99E-06	8.37E-04	-1.18	-6.40	19p13.3

3.9 PTD versus tMLL

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	228083_at	CACNA2D4	-12.12	1.08E-09	1.24E-05	-1.44	-8.75	12p13.33
2	208116_s_at	MAN1A1	3.86	1.69E-09	1.29E-05	1.37	8.74	6q22
3	214789_x_at	SRP46	2.22	3.48E-11	8.01E-07	1.20	8.56	11q22
4	200829_x_at	ZNF207	1.65	8.45E-09	2.56E-05	1.18	7.80	17q11.2
5	201152_s_at	MBNL1	-1.87	3.73E-09	1.71E-05	-1.09	-7.51	3q25
6	205601_s_at	HOXB5	3.26	1.43E-07	1.00E-04	1.32	7.48	17q21.3
7	220306_at	FLJ20202	3.78	6.16E-08	8.34E-05	1.17	7.36	1p11.1

8	218376_s_at	MICAL	-4.47	1.93E-08	3.70E-05	-1.10	-7.28	6q21
9	226580_at	BRMS1	1.96	8.23E-09	2.56E-05	1.04	7.26	14q13.1
10	201105_at	LGALS1	-3.24	3.37E-09	1.71E-05	-1.01	-7.19	22q13.1
11	201151_s_at	MBNL1	-2.33	2.47E-08	4.07E-05	-1.07	-7.13	3q25
12	205453_at	HOXB2	11.71	4.70E-07	1.86E-04	1.28	7.02	17q21-q22
13	219360_s_at	TRPM4	-78.99	1.34E-07	1.00E-04	-1.29	-6.99	19q13.33
14	228334_x_at	KIAA1712	1.86	8.90E-09	2.56E-05	0.98	6.98	4q34
15	204082_at	PBX3	-3.01	2.43E-08	4.07E-05	-1.02	-6.98	9q33-q34
16	218453_s_at	C6orf35	1.56	1.55E-08	3.58E-05	0.99	6.94	6q25.3
17	213159_at	PCNX	-2.47	1.15E-08	2.93E-05	-0.96	-6.87	14q24.1
18	227798_at		6.82	3.38E-07	1.68E-04	1.09	6.77	
19	201754_at	COX6C	-1.55	1.93E-08	3.70E-05	-0.95	-6.75	8q22-q23
20	232424_at	PRDM16	13.67	1.05E-06	2.79E-04	1.32	6.75	1p36.23-p33
21	201738_at	GC20	1.56	9.92E-08	9.93E-05	0.99	6.68	3p21.33
22	205366_s_at	HOXB6	25.13	1.29E-06	3.02E-04	1.31	6.65	17q21.3
23	225974_at	DKFZp762C1112	4.46	1.49E-07	1.00E-04	0.99	6.63	8q21.3
24	232919_at		2.17	1.07E-07	9.93E-05	0.96	6.56	
25	213737_x_at		-1.86	4.37E-08	6.28E-05	-0.93	-6.56	
26	200742_s_at	CLN2	-1.91	3.55E-08	5.45E-05	-0.92	-6.55	11p15
27	221823_at	LOC90355	2.34	2.97E-07	1.68E-04	1.00	6.54	5q21.1
28	212174_at	AK2	-2.78	1.05E-07	9.93E-05	-0.96	-6.54	1p34
29	209605_at	TST	-3.51	8.04E-08	9.93E-05	-0.95	-6.54	22q13.1
30	226278_at	DKFZp313A2432	2.51	1.10E-07	9.93E-05	0.95	6.53	11p14.2
31	230667_at		1.53	1.38E-07	1.00E-04	0.95	6.51	
32	222761_at	BIVM	2.73	3.08E-07	1.68E-04	0.99	6.51	13q32-q33.1
33	225464_at	C14orf31	2.61	9.25E-08	9.93E-05	0.93	6.48	14q21.3
34	202318_s_at	SUSP1	-2.08	1.15E-07	9.93E-05	-0.94	-6.45	6q13-q14.3
35	232038_at		2.51	3.16E-07	1.68E-04	0.97	6.44	
36	228652_at	FLJ38288	1.81	1.17E-07	9.93E-05	0.93	6.44	19q13.43
37	205600_x_at	HOXB5	2.14	1.49E-06	3.20E-04	1.13	6.43	17q21.3
38	229143_at	CNOT3	1.91	1.52E-07	1.00E-04	0.93	6.42	19q13.4
39	221760_at	MAN1A1	4.55	1.11E-06	2.81E-04	1.07	6.42	6q22
40	213258_at		8.86	1.87E-06	3.48E-04	1.15	6.39	
41	213152_s_at	SRP46	2.59	3.91E-07	1.71E-04	0.96	6.37	11q22
42	227400_at	NFIX	4.61	6.59E-07	2.14E-04	1.00	6.37	19p13.3
43	230006_s_at	DKFZp313A2432	2.41	2.27E-07	1.41E-04	0.92	6.33	11p14.2
44	221235_s_at		1.99	9.97E-07	2.73E-04	1.01	6.32	
45	218718_at	PDGFC	3.45	8.73E-08	9.93E-05	0.88	6.29	4q32
46	216941_s_at	TAF1B	-1.80	8.73E-08	9.93E-05	-0.88	-6.29	2p25
47	228974_at		3.57	1.56E-06	3.22E-04	1.05	6.28	
48	228760_at		2.74	1.32E-07	1.00E-04	0.89	6.28	
49	244103_at		2.45	8.00E-07	2.36E-04	0.97	6.26	
50	226517_at	BCAT1	6.88	2.15E-06	3.82E-04	1.08	6.24	12pter-q12

3.10 inv3 versus t(15;17)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	212953_x_at	CALR	-5.95	2.17E-14	5.07E-11	-3.69	-18.88	19p13.3-p13.2
2	205382_s_at	DF	-12.24	2.37E-15	7.12E-12	-3.43	-18.68	19p13.3
3	203948_s_at	MPO	-9.29	4.98E-19	1.05E-14	-3.14	-18.57	17q23.1
4	203949_at	MPO	-6.22	1.52E-17	1.60E-13	-3.05	-17.82	17q23.1
5	200654_at	P4HB	-3.78	4.67E-17	3.27E-13	-2.71	-16.03	17q25
6	214450_at	CTSW	-8.62	1.58E-13	2.89E-10	-2.90	-15.67	11q13.1
7	231736_x_at	MGST1	-6.90	6.57E-16	2.30E-12	-2.57	-15.09	12p12.3-p12.1
8	224918_x_at	MGST1	-6.02	2.58E-16	1.15E-12	-2.54	-15.02	12p12.3-p12.1
9	206871_at	ELA2	-6.28	2.73E-16	1.15E-12	-2.54	-15.00	19p13.3
10	214575_s_at	AZU1	-12.19	2.49E-13	3.73E-10	-2.58	-14.34	19p13.3
11	205624_at	CPA3	-21.54	5.79E-12	5.79E-09	-2.85	-14.33	3q21-q25
12	208689_s_at	RPN2	-2.77	3.65E-15	9.58E-12	-2.43	-14.27	20q12-q13.1
13	238022_at		-8.14	1.08E-12	1.33E-09	-2.28	-12.89	
14	38487_at	STAB1	-5.21	5.94E-13	8.31E-10	-2.23	-12.76	3p21.31
15	221004_s_at	ITM2C	-4.36	8.93E-14	1.88E-10	-2.12	-12.49	2q37
16	217716_s_at	SEC61A1	-2.51	1.65E-13	2.89E-10	-2.09	-12.25	3q21.3
17	221739_at	IL27w	-2.24	2.31E-13	3.73E-10	-2.06	-12.11	19p13.3
18	233072_at	KIAA1857	-10.04	1.05E-10	5.14E-08	-2.37	-12.06	9q34
19	208852_s_at	CANX	-2.94	3.24E-12	3.78E-09	-2.07	-11.86	5q35
20	220798_x_at	FLJ11535	-5.26	7.78E-12	6.81E-09	-2.05	-11.62	19p13.3
21	217225_x_at	LOC283820	-2.41	9.52E-13	1.25E-09	-1.94	-11.43	16p13.13
22	208730_x_at	RAB2	2.53	8.63E-10	3.12E-07	2.18	11.42	8q12.1
23	203675_at	NUCB2	-3.92	6.96E-12	6.65E-09	-2.00	-11.42	11p15.1-p14
24	201004_at	SSR4	-2.77	1.64E-11	1.15E-08	-2.00	-11.33	Xq28
25	210788_s_at	retSDR4	-2.65	7.69E-12	6.81E-09	-1.95	-11.22	14q22.3
26	202759_s_at	AKAP2	-4.78	2.58E-11	1.69E-08	-1.98	-11.15	9q31-q33
27	209619_at	CD74	4.57	1.47E-11	1.14E-08	1.92	11.07	5q32
28	214315_x_at	CALR	-3.14	2.25E-11	1.52E-08	-1.93	-11.00	19p13.3-p13.2
29	229168_at	DKFZp434K0621	-5.62	4.18E-10	1.72E-07	-2.12	-10.99	5q35.3
30	211990_at	HLA-DPA1	12.02	1.70E-08	3.31E-06	2.38	10.92	6p21.3
31	214797_s_at	PCTK3	6.22	2.95E-09	8.48E-07	2.12	10.91	1q31-q32
32	211709_s_at	SCGF	-5.08	3.77E-12	3.96E-09	-1.80	-10.65	19q13.3
33	200068_s_at - HG-U133A	CANX	-1.76	3.59E-12	3.96E-09	-1.79	-10.61	5q35
34	206914_at	CRTAM	6.82	3.01E-09	8.54E-07	1.99	10.50	11q22-q23
35	204897_at	PTGER4	5.48	3.25E-10	1.37E-07	1.87	10.44	5p13.1
36	221253_s_at	MGC3178	-3.45	5.95E-11	3.62E-08	-1.81	-10.36	6p24.3
37	225010_at	D10S170	2.56	2.69E-11	1.71E-08	1.77	10.33	10q21
38	210140_at	CST7	-8.79	1.17E-09	4.09E-07	-1.98	-10.32	20p11.21
39	226905_at		-1.96	8.40E-11	4.20E-08	-1.78	-10.24	
40	200652_at	SSR2	-1.91	1.02E-11	8.61E-09	-1.73	-10.22	1q21-q23

41	33323_r_at	SFN	1.93	1.07E-11	8.68E-09	1.73	10.21	1p35.3
42	227353_at	EVER2	5.28	1.34E-08	2.75E-06	2.02	10.17	17q25.3
43	224839_s_at	GPT2	-6.13	8.34E-11	4.20E-08	-1.77	-10.15	16q12.1
44	200068_s_at - HG-U133B	CANX	-1.67	1.62E-11	1.15E-08	-1.72	-10.14	5q35
45	209215_at	TETRAN	-3.38	1.52E-11	1.14E-08	-1.72	-10.14	4p16.3
46	205614_x_at	MST1	-8.62	3.49E-09	9.53E-07	-2.00	-9.99	3p21
47	241383_at		-4.56	2.13E-09	6.47E-07	-1.87	-9.85	
48	214317_x_at	RPS9	2.30	1.38E-09	4.55E-07	1.77	9.82	19q13.4
49	202487_s_at	H2AV	-2.25	6.02E-11	3.62E-08	-1.64	-9.66	7p13
50	204661_at	CDW52	22.88	1.06E-07	1.35E-05	2.16	9.63	1p36

3.11 inv3 versus t(821)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	-5.65	7.52E-13	1.81E-08	-2.11	-12.02	17q23.1
2	211084_x_at	PRKCN	5.87	3.47E-10	2.79E-06	1.89	10.40	2p21
3	233955_x_at	HSPC195	5.22	3.15E-08	8.44E-05	2.17	10.18	5q31.3
4	225010_at	D10S170	2.88	2.98E-11	3.60E-07	1.75	10.06	10q21
5	203948_s_at	MPO	-6.72	6.92E-10	4.17E-06	-1.71	-9.50	17q23.1
6	201281_at	ADRM1	-2.23	1.63E-09	7.87E-06	-1.63	-9.09	20q13.33
7	217963_s_at	NGFRAP1	29.06	4.70E-07	3.72E-04	2.04	8.66	Xq22.1
8	217226_s_at	BA108L7.2	3.73	5.93E-08	1.43E-04	1.66	8.63	10q24.31
9	219478_at	WFDC1	-12.65	9.84E-08	1.98E-04	-1.72	-8.45	16q24.3
10	224516_s_at	HSPC195	5.79	5.70E-07	3.72E-04	1.91	8.42	5q31.3
11	231180_at		-2.39	2.87E-09	1.15E-05	-1.47	-8.39	
12	228827_at		-99.36	2.41E-07	3.23E-04	-1.91	-8.24	
13	222996_s_at	HSPC195	4.30	1.07E-06	5.36E-04	1.78	7.97	5q31.3
14	212423_at	FLJ90798	4.16	7.34E-08	1.61E-04	1.47	7.96	10q22.3
15	230259_at		-1.94	2.68E-08	8.08E-05	-1.41	-7.87	
16	220974_x_at	BA108L7.2	5.01	4.47E-07	3.72E-04	1.57	7.86	10q24.31
17	230659_at	KIAA0212	-2.16	1.23E-07	2.29E-04	-1.47	-7.79	3p26.1
18	202759_s_at	AKAP2	-5.05	2.41E-07	3.23E-04	-1.52	-7.74	9q31-q33
19	205529_s_at	CBFA2T1	-14.01	5.55E-07	3.72E-04	-1.74	-7.73	8q22
20	213716_s_at	SECTM1	4.82	2.88E-07	3.30E-04	1.42	7.55	17q25
21	206478_at	KIAA0125	23.37	2.67E-06	8.04E-04	1.89	7.54	14q32.33
22	219165_at	PDLIM2	3.74	6.52E-07	4.03E-04	1.46	7.47	8p21.2
23	211709_s_at	SCGF	-3.56	2.43E-08	8.08E-05	-1.29	-7.41	19q13.3
24	212895_s_at	ABR	3.07	3.51E-07	3.53E-04	1.38	7.36	17p13.3
25	203820_s_at	KOC1	4.07	2.40E-06	7.71E-04	1.56	7.29	7p11
26	206295_at	IL18	3.55	2.33E-06	7.62E-04	1.53	7.25	11q22.2-q22.3
27	210150_s_at	LAMA5	-4.29	4.79E-07	3.72E-04	-1.38	-7.22	20q13.2-q13.3
28	201243_s_at	ATP1B1	5.05	2.16E-06	7.35E-04	1.49	7.20	1q22-q25
29	202006_at	PTPN12	2.72	7.49E-07	4.41E-04	1.37	7.18	7q11.23
30	202887_s_at	RTP801	4.33	1.63E-06	6.56E-04	1.43	7.14	10pter-q26.12

31	207839_s_at	LOC51754	3.10	2.62E-07	3.30E-04	1.28	7.08	9p13.1
32	201938_at	CDK2AP1	2.04	1.33E-07	2.29E-04	1.25	7.07	12q24.31
33	214042_s_at	RPL22	1.48	8.29E-07	4.76E-04	1.33	7.04	1p36.3-p36.2
34	226865_at		8.77	5.57E-06	1.18E-03	1.65	7.01	
35	222955_s_at	HT011	-2.21	5.13E-07	3.72E-04	-1.31	-7.01	Xq26.1
36	242621_at	FLJ32468	-1.60	3.47E-07	3.53E-04	-1.28	-7.00	7q22.1
37	223534_s_at	RPS6KL1	-2.19	3.25E-07	3.53E-04	-1.28	-7.00	14q24.2
38	215051_x_at	AIF1	2.61	2.78E-07	3.30E-04	1.26	6.99	6p21.3
39	231334_at		-3.75	8.70E-07	4.86E-04	-1.35	-6.98	
40	213908_at		4.04	2.34E-06	7.62E-04	1.38	6.94	
41	204494_s_at	DKFZP434H132	5.00	5.81E-06	1.22E-03	1.57	6.92	15q22.33
42	212953_x_at	CALR	-2.43	1.33E-06	5.73E-04	-1.37	-6.92	19p13.3-p13.2
43	228058_at	LOC124220	-2.64	5.60E-07	3.72E-04	-1.28	-6.91	16p13.3
44	227620_at		3.61	5.09E-07	3.72E-04	1.25	6.87	
45	221458_at	HTR1F	2.61	1.74E-06	6.76E-04	1.32	6.86	3p12
46	221773_at		3.67	1.02E-06	5.26E-04	1.28	6.85	
47	210613_s_at	SYNGR1	-2.93	1.84E-07	2.96E-04	-1.20	-6.83	22q13.1
48	214807_at		2.96	2.54E-06	8.04E-04	1.35	6.83	
49	229406_at		-11.96	2.16E-06	7.35E-04	-1.40	-6.81	
50	205528_s_at	CBFA2T1	-30.57	3.06E-06	8.69E-04	-1.54	-6.79	8q22

3.12 inv3 versus tMLL

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204082_at	PBX3	-8.13	5.43E-11	4.44E-07	-1.62	-9.85	9q33-q34
2	233955_x_at	HSPC195	5.24	8.76E-09	7.67E-06	1.68	9.58	5q31.3
3	226789_at		-3.29	1.13E-11	2.40E-07	-1.47	-9.56	
4	214651_s_at	HOXA9	-4.39	1.96E-11	2.40E-07	-1.37	-9.06	7p15-p14
5	225344_at	ERAP140	4.30	2.49E-07	5.42E-05	1.75	8.68	6q22.33
6	236398_s_at		-6.51	6.25E-10	2.19E-06	-1.32	-8.42	
7	235753_at		-4.84	4.98E-10	2.03E-06	-1.30	-8.41	
8	210006_at	DKFZP564O243	-2.26	4.92E-10	2.03E-06	-1.29	-8.36	3p21.1
9	224516_s_at	HSPC195	6.41	2.69E-07	5.68E-05	1.59	8.32	5q31.3
10	222982_x_at	SLC38A2	1.92	1.09E-09	2.44E-06	1.29	8.32	12q
11	235199_at		3.81	2.04E-07	4.75E-05	1.54	8.30	
12	213893_x_at	PMS2L5	-2.33	3.45E-10	2.03E-06	-1.25	-8.22	7q11-q22
13	214643_x_at	BIN1	4.75	2.15E-07	4.88E-05	1.51	8.20	2q14
14	203733_at	MYLE	-2.90	7.44E-10	2.28E-06	-1.25	-8.16	16p13.2
15	209905_at	HOXA9	-6.88	1.31E-09	2.44E-06	-1.27	-8.14	7p15-p14
16	212782_x_at	POLR2J	-2.47	1.59E-09	2.44E-06	-1.24	-8.04	7q11.2
17	228083_at	CACNA2D4	-8.54	2.08E-09	2.83E-06	-1.26	-8.04	12p13.33
18	202961_s_at	ATP5J2	-2.29	1.53E-09	2.44E-06	-1.23	-8.03	7q22.1
19	225386_s_at	LOC92906	-6.33	1.09E-09	2.44E-06	-1.22	-7.98	2p22.2
20	212318_at	TRN-SR	-2.60	1.30E-09	2.44E-06	-1.21	-7.92	7q32.2
21	211978_x_at	PPIA	-1.66	4.91E-09	5.47E-06	-1.23	-7.89	7p13-p11.2

22	222996_s_at	HSPC195	4.55	5.97E-07	9.52E-05	1.52	7.89	5q31.3
23	223207_x_at	PHP14	-1.83	1.21E-09	2.44E-06	-1.17	-7.76	9q34.3
24	208116_s_at	MAN1A1	4.91	8.97E-07	1.19E-04	1.53	7.75	6q22
25	223703_at	CDA017	-3.77	6.76E-09	6.56E-06	-1.24	-7.75	10q23.1
26	211378_x_at	PPIA	-1.67	1.05E-08	8.33E-06	-1.21	-7.74	7p13-p11.2
27	200602_at	APP	9.66	7.49E-07	1.08E-04	1.47	7.70	21q21.3
28	212174_at	AK2	-3.81	4.84E-09	5.47E-06	-1.20	-7.70	1p34
29	214430_at	GLA	-2.12	1.56E-09	2.44E-06	-1.16	-7.68	Xq22
30	202053_s_at	ALDH3A2	-2.84	6.95E-09	6.56E-06	-1.21	-7.66	17p11.2
31	202054_s_at	ALDH3A2	-4.35	1.85E-09	2.67E-06	-1.16	-7.65	17p11.2
32	214453_s_at	IFI44	5.44	1.39E-06	1.62E-04	1.56	7.63	1p31.1
33	201293_x_at	PPIA	-1.61	1.25E-08	9.18E-06	-1.19	-7.61	7p13-p11.2
34	209836_x_at	MGC5178	-2.07	2.21E-09	2.85E-06	-1.15	-7.61	16p12.1
35	208967_s_at	AK2	-3.93	1.89E-08	1.13E-05	-1.23	-7.52	1p34
36	230051_at		4.17	4.75E-07	8.15E-05	1.31	7.43	
37	202605_at	GUSB	-3.22	6.78E-09	6.56E-06	-1.13	-7.38	7q21.11
38	225389_at	BTBD6	-2.28	4.68E-09	5.47E-06	-1.11	-7.35	14q32
39	219551_at	TRAITS	-3.19	1.15E-08	8.82E-06	-1.14	-7.34	3q13.33
40	201829_at	NET1	3.64	2.56E-06	2.40E-04	1.53	7.32	10p15
41	206478_at	KIAA0125	15.02	3.35E-06	2.89E-04	1.66	7.32	14q32.33
42	201186_at	LRPAP1	-3.24	1.57E-08	1.01E-05	-1.14	-7.31	4p16.3
43	219126_at	XAP135	-1.82	5.33E-09	5.68E-06	-1.10	-7.31	6q27
44	223328_at	MGC3195	-2.10	9.36E-09	7.92E-06	-1.11	-7.30	7q22.1
45	211765_x_at	PPIA	-1.60	4.19E-08	1.88E-05	-1.15	-7.30	7p13-p11.2
46	205514_at	FLJ11191	4.23	1.61E-06	1.78E-04	1.40	7.29	19q13.41
47	215667_x_at	PMS2L5	-1.92	7.42E-09	6.74E-06	-1.10	-7.27	7q11-q22
48	212661_x_at		-1.59	4.26E-08	1.88E-05	-1.13	-7.21	
49	228652_at	FLJ38288	2.29	6.02E-07	9.52E-05	1.26	7.20	19q13.43
50	213908_at		-3.92	3.73E-08	1.83E-05	-1.16	-7.20	

3.13 t(15;17) versus t(821)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214450_at	CTSW	27.45	1.67E-13	5.02E-09	3.57	17.69	11q13.1
2	38487_at	STAB1	19.09	4.71E-13	7.07E-09	3.25	16.45	3p21.31
3	209732_at	CLECSF2	-30.85	1.79E-11	4.88E-08	-3.32	-15.30	12p13-p12
4	211990_at	HLA-DPA1	-11.19	1.56E-11	4.67E-08	-2.71	-14.09	6p21.3
5	224839_s_at	GPT2	12.86	6.29E-11	1.35E-07	2.35	12.29	16q12.1
6	212509_s_at		9.95	9.86E-11	1.96E-07	2.36	12.15	
7	226878_at		-5.69	4.61E-10	5.32E-07	-2.25	-11.62	
8	204150_at	STAB1	20.67	3.59E-10	4.49E-07	2.35	11.56	3p21.31
9	201596_x_at	KRT18	20.76	3.10E-10	4.05E-07	2.28	11.50	12q13
10	205349_at	GNA15	3.49	3.36E-11	8.40E-08	1.98	11.31	19p13.3
11	205663_at	PCBP3	4.59	8.09E-12	3.47E-08	1.92	11.31	21q22.3

12	221004_s_at	ITM2C	3.23	8.52E-13	8.53E-09	1.85	11.27	2q37
13	212953_x_at	CALR	2.45	1.20E-12	8.99E-09	1.76	10.80	19p13.3-p13.2
14	217478_s_at	HLA-DMA	-5.51	4.09E-10	4.91E-07	-1.94	-10.73	6p21.3
15	227326_at		5.33	2.87E-10	3.99E-07	1.88	10.49	
16	228113_at	STAT3	-5.22	9.54E-10	8.68E-07	-1.92	-10.46	17q21
17	217716_s_at	SEC61A1	2.04	7.06E-12	3.47E-08	1.71	10.39	3q21.3
18	208826_x_at	HINT1	1.40	4.69E-12	2.81E-08	1.68	10.32	5q31.2
19	200986_at	SERPING1	9.53	1.51E-09	1.26E-06	1.97	10.29	11q12-q13.1
20	201137_s_at	HLA-DPB1	-13.90	1.17E-08	6.03E-06	-2.10	-10.00	6p21.3
21	208689_s_at	RPN2	1.78	1.23E-11	4.60E-08	1.60	9.83	20q12-q13.1
22	204316_at	RGS10	-2.46	9.39E-10	8.68E-07	-1.71	-9.76	10q25
23	209619_at	CD74	-4.69	2.02E-10	3.19E-07	-1.65	-9.75	5q32
24	204670_x_at	HLA-DRB5	-5.88	5.55E-10	5.74E-07	-1.68	-9.73	6p21.3
25	201522_x_at	SNRPN	-3.71	1.47E-11	4.67E-08	-1.58	-9.71	15q12
26	211991_s_at	HLA-DPA1	-17.64	1.79E-08	8.26E-06	-2.00	-9.66	6p21.3
27	205614_x_at	MST1	7.48	3.65E-09	2.28E-06	1.82	9.65	3p21
28	209021_x_at	KIAA0652	4.23	5.35E-11	1.23E-07	1.59	9.63	11p11.12
29	200953_s_at	CCND2	2.65	5.21E-10	5.74E-07	1.64	9.52	12p13
30	209312_x_at	HLA-DRB1	-7.00	4.59E-09	2.76E-06	-1.73	-9.47	6p21.3
31	208852_s_at	CANX	2.27	1.04E-10	1.96E-07	1.56	9.42	5q35
32	201425_at	ALDH2	5.10	1.10E-09	9.46E-07	1.60	9.25	12q24.2
33	201136_at	PLP2	2.70	2.93E-10	3.99E-07	1.54	9.23	Xp11.23
34	201952_at	ALCAM	4.55	2.64E-09	1.80E-06	1.63	9.21	3q13.1
35	218795_at	ACP6	-2.74	3.46E-09	2.21E-06	-1.61	-9.16	1q21
36	208306_x_at	HLA-DRB4	-7.29	1.08E-08	5.68E-06	-1.69	-9.14	6p21.3
37	206940_s_at	POU4F1	-45.95	7.19E-08	1.96E-05	-2.09	-8.99	13q21.1-q22
38	223321_s_at	FGFRL1	3.71	4.93E-09	2.90E-06	1.59	8.94	4p16
39	201923_at	PRDX4	-5.97	1.90E-08	8.63E-06	-1.67	-8.94	Xp22.13
40	215193_x_at	HLA-DRB1	-7.01	5.77E-09	3.27E-06	-1.57	-8.92	6p21.3
41	207721_x_at	HINT1	1.51	1.53E-10	2.70E-07	1.45	8.89	5q31.2
42	238022_at		3.92	1.64E-10	2.74E-07	1.43	8.81	
43	227353_at	EVER2	-3.90	8.45E-09	4.61E-06	-1.56	-8.81	17q25.3
44	224451_x_at	ARHGAP9	-2.71	7.08E-10	6.86E-07	-1.45	-8.77	12q14
45	209344_at	TPM4	6.76	2.31E-08	9.73E-06	1.68	8.76	19p13.1
46	211474_s_at	SERPINB6	-5.75	5.58E-08	1.75E-05	-1.73	-8.75	6p25
47	201360_at	CST3	4.40	2.09E-09	1.53E-06	1.48	8.70	20p11.21
48	201894_s_at	DCN	1.99	2.33E-10	3.49E-07	1.41	8.69	12q13.2
49	202732_at	PKIG	2.65	2.59E-09	1.80E-06	1.48	8.66	20q12-q13.1
50	211341_at	POU4F1	-309.60	1.24E-07	2.80E-05	-2.02	-8.65	13q21.1-q22

3.14 t(15;17) versus tMLL

#	affy id	HUGO name	fc	p	q	stn	t	Map Location

1	221004_s_at	ITM2C	10.63	1.44E-14	5.99E-11	2.85	16.93 2q37
2	38487_at	STAB1	16.43	2.86E-13	5.50E-10	2.90	16.09 3p21.31
3	205624_at	CPA3	36.17	5.95E-12	7.42E-09	3.00	14.74 3q21-q25
4	203948_s_at	MPO	5.78	4.02E-19	1.00E-14	2.09	14.65 17q23.1
5	214651_s_at	HOXA9	-236.49	2.65E-14	9.43E-11	-2.61	-14.18 7p15-p14
6	212953_x_at	CALR	3.23	1.31E-14	5.99E-11	2.20	14.16 19p13.3-p13.2
7	214450_at	CTSW	6.15	3.95E-14	1.23E-10	2.18	13.92 11q13.1
8	200953_s_at	CCND2	6.53	2.29E-12	3.11E-09	2.32	13.58 12p13
9	203949_at	MPO	4.10	5.38E-16	4.47E-12	1.82	12.55 17q23.1
10	206871_at	ELA2	4.27	1.94E-16	2.43E-12	1.79	12.53 19p13.3
11	238022_at		6.11	2.20E-12	3.11E-09	1.97	12.29
12	233072_at	KIAA1857	12.53	6.26E-11	3.19E-08	2.25	12.28 9q34
13	213147_at	HOXA10	-23.65	1.43E-12	2.37E-09	-2.06	-11.90 7p15-p14
14	204150_at	STAB1	20.35	3.43E-10	1.16E-07	2.25	11.53 3p21.31
15	209448_at	HTATIP2	-10.10	2.27E-12	3.11E-09	-1.86	-11.35 11p15.1
16	200951_s_at	CCND2	7.49	1.92E-10	7.62E-08	1.99	11.24 12p13
17	210788_s_at	retSDR4	2.54	1.20E-11	1.17E-08	1.77	11.17 14q22.3
18	201029_s_at	CD99	2.20	1.43E-14	5.99E-11	1.57	11.01 Xp22.32
19	205663_at	PCBP3	3.90	2.95E-11	2.05E-08	1.77	11.01 21q22.3
20	205349_at	GNA15	4.35	9.31E-13	1.66E-09	1.64	10.95 19p13.3
21	212509_s_at		6.22	1.29E-10	5.66E-08	1.84	10.93
22	206761_at	TACTILE	29.33	1.19E-09	3.13E-07	2.28	10.90 3q13.13
23	200952_s_at	CCND2	4.35	2.19E-10	8.42E-08	1.86	10.85 12p13
24	201596_x_at	KRT18	10.40	5.91E-10	1.85E-07	1.98	10.82 12q13
25	217848_s_at	PP	-3.83	1.98E-13	4.18E-10	-1.59	-10.82 10q11.1-q24
26	235753_at		-16.42	1.82E-11	1.42E-08	-1.91	-10.74
27	206847_s_at	HOXA7	-9.06	7.47E-12	8.47E-09	-1.72	-10.70 7p15-p14
28	201522_x_at	SNRPN	-4.71	6.74E-14	1.87E-10	-1.53	-10.64 15q12
29	225532_at	LOC91768	5.85	7.26E-10	2.16E-07	1.93	10.63 18q11.1
30	205771_s_at	AKAP7	-9.87	9.16E-12	9.94E-09	-1.70	-10.58 6q23
31	231736_x_at	MGST1	2.94	2.01E-13	4.18E-10	1.53	10.56 12p12.3-p12.1
32	213587_s_at	LOC155066	-7.85	2.11E-11	1.58E-08	-1.79	-10.53 7q36.1
33	213150_at	HOXA10	-43.13	3.71E-11	2.32E-08	-1.85	-10.41 7p15-p14
34	224918_x_at	MGST1	2.74	1.26E-13	3.15E-10	1.48	10.35 12p12.3-p12.1
35	225386_s_at	LOC92906	-36.93	5.16E-11	2.86E-08	-1.80	-10.23 2p22.2
36	209905_at	HOXA9	-700.51	6.49E-11	3.24E-08	-1.89	-10.18 7p15-p14
37	221253_s_at	MGC3178	3.07	1.58E-10	6.70E-08	1.60	10.05 6p24.3
38	204082_at	PBX3	-8.66	4.80E-11	2.73E-08	-1.63	-9.98 9q33-q34
39	218404_at	SNX10	-6.62	3.43E-11	2.19E-08	-1.59	-9.95 7p15.2
40	225653_at		2.34	1.14E-09	3.02E-07	1.64	9.75
41	217716_s_at	SEC61A1	1.98	7.04E-12	8.37E-09	1.43	9.71 3q21.3
42	219837_s_at	C17	88.02	8.44E-09	1.29E-06	2.06	9.69 4p16-p15
43	202265_at	BMI1	-4.05	2.73E-11	1.95E-08	-1.48	-9.68 10p11.23
44	212813_at	JAM3	5.10	3.78E-09	7.19E-07	1.74	9.64 11q25
45	241383_at		4.10	4.07E-09	7.52E-07	1.74	9.61

46	210140_at	CST7	6.56	1.35E-09	3.32E-07	1.59	9.54	20p11.21
47	202746_at	ITM2A	18.72	8.03E-09	1.26E-06	1.84	9.53	Xq13.3-Xq21.2
48	225570_at	SLC41A1	-3.47	1.50E-11	1.34E-08	-1.40	-9.47	1q32.1
49	211474_s_at	SERPINB6	-4.69	7.52E-11	3.54E-08	-1.47	-9.45	6p25
50	208852_s_at	CANX	2.24	7.24E-11	3.48E-08	1.43	9.44	5q35

3.15 t(821) versus tMLL

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214651_s_at	HOXA9	-202.90	2.68E-14	7.75E-10	-2.60	-14.17	7p15-p14
2	221581_s_at	WBSCR5	-9.72	2.43E-13	3.51E-09	-2.04	-12.41	7q11.23
3	213147_at	HOXA10	-14.91	2.06E-12	1.19E-08	-1.91	-11.48	7p15-p14
4	201105_at	LGALS1	-6.99	4.93E-13	4.74E-09	-1.67	-10.99	22q13.1
5	235753_at		-14.41	2.17E-11	7.40E-08	-1.87	-10.63	
6	206847_s_at	HOXA7	-7.77	1.54E-11	6.34E-08	-1.77	-10.59	7p15-p14
7	213150_at	HOXA10	-51.45	3.41E-11	8.96E-08	-1.87	-10.45	7p15-p14
8	209905_at	HOXA9	-608.56	6.52E-11	1.52E-07	-1.89	-10.18	7p15-p14
9	227853_at		-3.66	1.21E-12	8.72E-09	-1.47	-9.96	
10	210314_x_at	TNFSF13	-4.46	2.53E-11	7.40E-08	-1.42	-9.38	17p13.1
11	213908_at		-15.84	3.74E-10	5.69E-07	-1.63	-9.33	
12	203949_at	MPO	3.73	1.28E-11	6.15E-08	1.34	9.15	17q23.1
13	216417_x_at	HOXB9	-3.57	2.56E-11	7.40E-08	-1.36	-9.13	17q21.3
14	228058_at	LOC124220	6.98	1.09E-09	9.83E-07	1.42	8.99	16p13.3
15	209500_x_at	TNFSF13	-3.79	1.57E-10	3.03E-07	-1.39	-8.99	17p13.1
16	204082_at	PBX3	-6.21	1.07E-10	2.21E-07	-1.37	-8.98	9q33-q34
17	206940_s_at	POU4F1	42.83	7.36E-08	2.10E-05	2.07	8.97	13q21.1-q22
18	225245_x_at	H2AFJ	-5.25	2.55E-10	4.61E-07	-1.37	-8.84	12p12
19	228083_at	CACNA2D4	-12.80	1.04E-09	9.71E-07	-1.50	-8.84	12p13.33
20	211341_at	POU4F1	239.48	1.25E-07	2.94E-05	2.01	8.64	13q21.1-q22
21	228365_at	LOC144402	-7.69	1.63E-09	1.38E-06	-1.44	-8.60	12q11
22	202746_at	ITM2A	7.78	2.76E-08	1.01E-05	1.49	8.56	Xq13.3-Xq21.2
23	212459_x_at	SUCLG2	-3.83	6.86E-11	1.52E-07	-1.25	-8.53	3p14.2
24	218404_at	SNX10	-4.04	4.74E-10	6.85E-07	-1.31	-8.53	7p15.2
25	201944_at	HEXB	-3.46	1.87E-09	1.46E-06	-1.39	-8.47	5q13
26	223562_at	PARVG	-3.25	6.78E-10	8.16E-07	-1.30	-8.43	22q13.2-q13
27	204202_at	KIAA1023	-3.48	6.42E-10	8.06E-07	-1.28	-8.38	7p22.3
28	212423_at	FLJ90798	-5.34	6.18E-10	8.06E-07	-1.28	-8.37	10q22.3
29	205639_at	AOAH	-5.26	7.95E-10	8.83E-07	-1.26	-8.27	7p14-p12
30	224301_x_at	H2AFJ	-4.35	8.84E-10	9.12E-07	-1.26	-8.26	12p12
31	228827_at		114.73	2.37E-07	4.10E-05	1.93	8.26	
32	201850_at	CAPG	-8.11	4.48E-09	2.88E-06	-1.40	-8.24	2cen-q24
33	208890_s_at	PLXNB2	-4.00	9.67E-10	9.31E-07	-1.24	-8.17	22q13.33
34	221841_s_at		-4.00	3.65E-10	5.69E-07	-1.20	-8.13	

35	214835_s_at	SUCLG2	-4.02	7.31E-10	8.45E-07	-1.21	-8.10 3p14.2
36	224415_s_at	HINT2	-2.05	3.35E-10	5.69E-07	-1.18	-8.08 9p13.1
37	201281_at	ADRM1	1.93	1.65E-08	7.22E-06	1.29	8.04 20q13.33
38	218217_at	RISC	-5.08	3.89E-09	2.69E-06	-1.28	-8.04 17q23.1
39	238756_at		-4.18	2.31E-09	1.76E-06	-1.24	-8.01
40	242931_at		-3.58	1.78E-09	1.43E-06	-1.22	-7.99
41	204069_at	MEIS1	-17.90	1.09E-08	5.54E-06	-1.42	-7.96 2p14-p13
42	241370_at		-3.07	3.39E-09	2.45E-06	-1.24	-7.96
43	225386_s_at	LOC92906	-6.56	9.62E-10	9.31E-07	-1.17	-7.91 2p22.2
44	215772_x_at	SUCLG2	-4.01	5.45E-10	7.49E-07	-1.15	-7.88 3p14.2
45	229002_at	MGC20262	4.77	9.02E-08	2.39E-05	1.35	7.88 9q34.3
46	219478_at	WFDC1	7.40	2.12E-07	3.90E-05	1.44	7.84 16q24.3
47	213737_x_at		-1.99	8.41E-10	9.00E-07	-1.14	-7.80
48	221760_at	MAN1A1	12.13	4.59E-07	6.50E-05	1.62	7.78 6q22
49	219271_at	GalNac-T10	6.98	2.26E-07	4.00E-05	1.41	7.76 2p23.1
50	231334_at		5.10	2.43E-07	4.16E-05	1.42	7.75

Claims

1. A method for distinguishing MLL-PTD-positive AML from other AML subtypes in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, and/or 3,

wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1

is indicative for the presence of PTD (MLL-PTD-positive AML with normal karyotype) when PTD is distinguished from AML_NK (MLL-PTD-negative AML with normal karyotype),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 12, 14, 15, 16, 18, 19, 20, 21, 22, 23, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 44, 45, 47, 48, 49, and/or 50 of Table 2.1, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 10, 13, 17, 24, 25, 41, 43, and/or 46, of Table 2.1,

is indicative for M4eo when M4eo is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 26, 28, 29, 31, 32, 33, 34, 35, 36, 38, 39, 41, 42, 44, 45, 46, 48, 49, and/or 50 of Table 2.2, and/or

a higher expression of 5, 13, 18, 27, 30, 37, 40, 43, and/or 47, of Table 2.2

is indicative for PTD when PTD is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 49, and/or 50 of Table 2.3, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 34, and/or 48, of Table 2.3

is indicative for inv3 when inv3 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 5, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 23, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 41, 42, 43, 44, 45, 46, 47, 48, and/or 50 of Table 2.4, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 4, 6, 7, 8, 22, 24, 40, and/or 49, of Table 2.4

is indicative for t(15;17) when t(15;17) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 2.5

is indicative for t(8;21) when t(8;21) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 43, 45, 46, 47, 48, 49, and/or 50 of Table 2.6, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 12, 15, 29, 41, and/or 44, of Table 2.6

is indicative for tMLL when tMLL is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 4, 5, 7, 10, 12, 13, 16, 17, 19, 23, 25, 30, 31, 32, 33, 34, 37, 41, 43, 45, 47, 48, and/or 50 of Table 3.1,and/or

a higher expression a polynucleotide defined by any of the numbers 3, 6, 8, 9, 11, 14, 15, 18, 20, 21, 22, 24, 26, 27, 28, 29, 35, 36, 38, 39, 40, 42, 44, 46, and/or 49, of Table 3.1,

is indicative for M4eo when M4eo is distinguished from PTD,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 5, 6, 9, 12, 23, 28, 38, 41, 44, 45, 46, and/or 47, of Table 3.2, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 7, 8, 10, 11, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 24, 25, 26, 27, 29, 30, 31, 32, 33, 34, 35, 36, 37, 39, 40, 42, 43, 48, 49, and/or 50 of Table 3.2,

is indicative for M4eo when M4eo is distinguished from inv3,

a lower expression of at least one polynucleotide defined by any of the numbers 2, 3, 4, 6, 11, 14, 20, 22, 26, 31, 32, 33, 34, 39, 40, 41, and/or 48, of Table 3.3, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 5, 7, 8, 9, 10, 12, 13, 15, 16, 17, 18, 19, 21, 23, 24, 25, 27, 28, 29, 30, 35, 36, 37, 38, 42, 43, 44, 45, 46, 47, 49, and/or 50 of Table 3.3,

is indicative for M4eo when M4eo is distinguished from t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 7, 31, 40, and/or 49, of Table 3.4, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20,

21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 32, 33, 34, 35, 36, 37, 38, 39, 41, 42, 43, 44, 45, 46, 47, 48, and/or 50 of Table 3.4

is indicative for M4eo when M4eo is distinguished from t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 3, 10, 14, 17, 18, 19, 21, 24, 25, 26, 31, 32, 34, 41, 44, and/or 50 of Table 3.5, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 2, 4, 5, 6, 7, 8, 9, 11, 12, 13, 15, 16, 20, 22, 23, 27, 28, 29, 30, 33, 35, 36, 37, 38, 39, 40, 42, 43, 45, 46, 47, 48, and/or 49, of Table 3.5

is indicative for M4eo when M4eo is distinguished from tMLL,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 4, 6, 9, 28, 30, 32, 35, 37, 44, 45, and/or 48, of Table 3.6, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 5, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 29, 31, 33, 34, 36, 38, 39, 40, 41, 42, 43, 46, 47, 49, and/or 50 of Table 3.6

is indicative for PTD when PTD is distinguished from inv3,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 6, 7, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 23, 27, 28, 29, 30, 31, 32, 33, 34, 36, 38, 39, 41, 43, 44, 45, 47, 48, and/or 50 of Table 3.7, and/or

a higher expression of polynucleotide defined by any of the numbers 5, 8, 9, 19, 21, 22, 24, 25, 26, 35, 37, 40, 42, 46, and/or 49, of Table 3.7,

is for PTD when PTD is distinguished from t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 7, 9, 10, 11, 13, 16, 20, 21, 22, 23, 30, 35, 36, 38, 42, 45, and/or 50 of Table 3.8, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 8, 12, 14, 15, 17, 18, 19, 24, 25, 26, 27, 28, 29, 31, 32, 33, 34, 37, 39, 40, 41, 43, 44, 46, 47, 48, and/or 49, of Table 3.8

is indicative for PTD when PTD is distinguished from t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 5, 8, 10, 11, 13, 15, 17, 19, 25, 26, 28, 29, 34, and/or 46, of Table 3.9, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 2, 3, 4, 6, 7, 9, 12, 14, 16, 18, 20, 21, 22, 23, 24, 27, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 47, 48, 49, and/or 50 of Table 3.9

is indicative for PTD when PTD is distinguished from tMLL,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 23, 24, 25, 26, 28, 29, 32, 33, 36, 38, 39, 40, 43, 44, 45, 46, 47, and/or 49, of Table 3.10, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 22, 27, 30, 31, 34, 35, 37, 41, 42, 48, and/or 50 of Table 3.10,

is indicative for inv(3) when inv(3) is distinguished from t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 5, 6, 9, 11, 12, 15, 17, 18, 19, 23, 27, 35, 36, 37, 39, 42, 43, 47, 49, and/or 50 of Table 3.11, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 2, 3, 4, 7, 8, 10, 13, 14, 16, 20, 21, 22, 24, 25, 26, 28, 29, 30, 31, 32, 33, 34, 38, 40, 41, 44, 45, 46, and/or 48, of Table 3.11

is indicative for inv(3) when inv(3) is distinguished from t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 3, 4, 6, 7, 8, 12, 14, 15, 16, 17, 18, 19, 20, 21, 23, 25, 26, 28, 29, 30, 31, 33, 34, 35, 37, 38, 39, 42, 43, 44, 45, 47, 48, and/or 50 of Table 3.12, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 2, 5, 9, 10, 11, 13, 22, 24, 27, 32, 36, 40, 41, 46, and/or 49, of Table 3.12

is indicative for inv(3) when inv(3) is distinguished from tMLL,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 3, 4, 7, 14, 16, 20, 22, 23, 24, 25, 26, 30, 35, 36, 37, 39, 40, 43, 44, 46, and/or 50 of Table 3.13, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 5, 6, 8, 9, 10, 11, 12, 13, 15, 17, 18, 19, 21, 27, 28, 29, 31, 32, 33, 34, 38, 41, 42, 45, 47, 48, and/or 49 of Table 3.13,

is indicative for t(15;17) when t(15;17) is distinguished from t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 13, 15, 25, 26, 27, 28, 30, 32, 33, 35, 36, 38, 39, 43, 48, and/or 49, of Table 3.14, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 29, 31, 34, 37, 40, 41, 42, 44, 45, 46, 47, and/or 50 of Table 3.14,

is indicative for t(15;17) when t(15;17) is distinguished from tMLL,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 15, 16, 18, 19, 21, 23, 24, 25, 26, 27, 28, 29, 30, 32, 33, 34, 35, 36, 38, 39, 40, 41, 42, 43, 44, 47, 48, of Table 3.15, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 12, 14, 17, 20, 22, 31, 37, 45, 46, 49, and/or 50 of Table 3.15, is indicative for t(8;21) when t(8;21) is distinguished from tMLL.

2. The method according to claim 1 wherein the polynucleotide is labelled.

3. The method according to claim 1 or 2, wherein the label is a luminescent, preferably a fluorescent label, an enzymatic or a radioactive label.

4. The method according at least one of the claims 1-3, wherein the expression level of at least two, preferably of at least ten, more preferably of at least 25, most preferably of 50 of the markers of at least one of the Table 1.1-3.15 is determined.

5. The method according to at least one of the claims 1-4, wherein the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold lower, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold lower in the first subtype.

6. The method according to at least one of the claims 1-4, wherein the expression level of markers expressed higher in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold higher, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold higher in the first subtype.

7. The method according to at least one of the claims 1-6, wherein the sample is from an individual having AML.

8. The method according to at least one of the claims 1-7, wherein at least one polynucleotide is in the form of a transcribed polynucleotide, or a portion thereof.

9. The method according to claim 8, wherein the transcribed polynucleotide is a mRNA or a cDNA.

10. The method according to claim 8 or 9, wherein the determining of the expression level comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions.

11. The method according to at least one of the claims 1-7, wherein at least one polynucleotide is in the form of a polypeptide, or a portion thereof.

12. The method according to claim 8, 9 or 12, wherein the determining of the expression level comprises contacting the polynucleotide or the polypeptide with a compound specifically binding to the polynucleotide or the polypeptide.

13. The method according to claim 12, wherein the compound is an antibody, or a fragment thereof.

14. The method according to at least one of the claims 1-13, wherein the method is carried out on an array.

15. The method according to at least one of the claims 1-14, wherein the method is carried out in a robotics system.

16. The method according to at least one of the claims 1-15, wherein the method is carried out using microfluidics.

17. Use of at least one marker as defined in at least one of the claims 1-3 for the manufacturing of a diagnostic for distinguishing MLL-PTD-positive AML from other AML subtypes.

18. The use according to claim 17 for distinguishing MLL-PTD-positive AML from other AML subtypes in an individual having AML.

19. A diagnostic kit containing at least one marker as defined in at least one of the claims 1-3 for distinguishing MLL-PTD-positive AML from other AML subtypes, in combination with suitable auxiliaries.

20. The diagnostic kit according to claim 19, wherein the kit contains a reference for the MLL-PTD-positive AML subtypes.

21. The diagnostic kit according to claim 20, wherein the reference is a sample or a data bank.

22. An apparatus for distinguishing MLL-PTD-positive AML from other AML subtypes in a sample containing a reference data bank.

23. The apparatus according to claim 22, wherein the reference data bank is obtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, 4, 5, 6 and/or 7, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

24. The apparatus according to claim 23, wherein the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines, and Feed-Forward Neural Networks, preferably Support Vector Machines.

25. The apparatus according to at least one of the claims 22-24, wherein the apparatus contains a control panel and/or a monitor.

26. A reference data bank for distinguishing MLL-PTD-positive AML from other AML subtypes obtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, 4, 5, 6 and/or 7, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

27. The reference data bank according to claim 26, wherein the reference data bank is backed up and/or contained in a computational memory chip.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
12 May 2005 (12.05.2005)

PCT

(10) International Publication Number
WO 2005/043162 A3

(51) International Patent Classification[7]: G01N 33/574, C12Q 1/68

(21) International Application Number:
PCT/EP2004/012464

(22) International Filing Date:
4 November 2004 (04.11.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
03025339.7 4 November 2003 (04.11.2003) EP

(71) Applicant *(for DE only)*: **ROCHE DIAGNOSTICS GMBH** [DE/DE]; Sandhofer Str. 116, 68305 Mannheim (DE).

(71) Applicant *(for all designated States except DE, US)*: **F.HOFFMANN-LA ROCHE AG** [CH/CH]; Grenzacherstrasse 124, CH-4070 Basel (CH).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **HAFERLACH, Torsten** [DE/DE]; Springerstrasse 8, 81477 München (DE). **DUGAS, Martin** [DE/DE]; Michael-Fischer-Platz 6, 94469 Deggendorf (DE). **KERN, Wolfgang** [DE/DE]; Hanfelder Strasse 101, 82319 Starnberg (DE). **KOHLMANN, Alexander** [DE/DE]; Schwarzstrasse 14, 92318 Neumarkt (DE). **SCHNITTGER, Susanne** [DE/DE]; Saalburgstrasse 2a, 81375 München (DE). **SCHOCH, Claudia** [DE/DE]; Springerstrasse 8, 81477 München (DE).

(74) Common Representative: **ROCHE DIAGNOSTICS GMBH**; C/O Burger Alexander, Patent Department (TR-E), Postfach 11 52, 82372 Penzberg (DE).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments*

(88) Date of publication of the international search report:
18 August 2005

(15) Information about Correction:
Previous Correction:
see PCT Gazette No. 27/2005 of 7 July 2005, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHOD FOR DISTINGUISHING MLL-PTD-POSITIVE AML FROM OTHER AML SUBTYPES

(57) Abstract: Disclosed is a method for distinguishing MLL-PTD-positive AML from other AML subtypes in a sample by determining the expression level of markers, as well as a diagnostic kit and an apparatus containing the markers.

WO 2005/043162 A3

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/012464

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 G01N33/574 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 G01N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, BIOSIS, WPI Data, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), SCHNITTGER SUSANNE ET AL: "Acute Myeloid Leukemia (AML) with Partial Tandem Duplication of the MLL-Gene (MLL-PTD) Can Be Discriminated from MLL-Translocations Based on Specific Gene Expression Profiles." XP002270207 Database accession no. PREV200300335802 abstract -/--	1-27

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
3 March 2005	09. 06. 2005

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Thumb, W

Form PCT/ISA/210 (second sheet) (January 2004)

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/012464

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	& BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 1202, 44th Annual Meeting of the American Society of Hematology;Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971 -----	
Y	SCHOCH CLAUDIA ET AL: "Acute myeloid leukemias with reciprocal rearrangements can be distinguished by specific gene expression profiles" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 99, no. 15, 23 July 2002 (2002-07-23), pages 10008-10013, XP002215484 ISSN: 0027-8424 the whole document in particular tables 1 and 2 -----	1-27
Y	WO 03/039443 A (DEUTSCHES KREBSFORSCH ;HAFERLACH TORSTEN (DE); EILS ROLAND (DE); K) 15 May 2003 (2003-05-15) the whole document in particular Examples 4, 6 and 7 -----	1-27
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), HAFERLACH TORSTEN ET AL: "Gene Expression Profiling Is Able To Reproduce Different Phenotypes in AML as Defined by the FAB Classification." XP002269981 Database accession no. PREV200300357598 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 731, 44th Annual Meeting of the American Society of Hematology;Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971 ----- -/--	1-27

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), NEBEN KAI ET AL: "Acute Myeloid Leukemia with Normal Karyotype and Mutation of the FLT3 or MLL Gene Are Characterized by Specific Gene Expression Profiles." XP002270208 Database accession no. PREV200300336869 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 2172, 44th Annual Meeting of the American Society of Hematology;Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971 -----	1-27
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2001 (2001-11-16), SCHNITTGER SUSANNE ET AL: "Partial tandem duplications (PTD) of the MLL gene: A study of 1603 patients reveals high frequency in secondary acute myeloid leukemia and low association with trisomy 11" XP002270209 Database accession no. PREV200200261466 abstract & BLOOD, vol. 98, no. 11 Part 1, 16 November 2001 (2001-11-16), page 801a, 43rd Annual Meeting of the American Society of Hematology, Part 1;Orlando, Florida, USA; December 07-11, 2001 ISSN: 0006-4971 -----	1-27
Y	KOHLMANN A ET AL: "MOLECULAR CHARACTERIZATION OF ACUTE LEUKEMIAS BY USE OF MICROARRAY TECHNOLOGY" GENES, CHROMOSOMES & CANCER, XX, XX, vol. 37, no. 4, August 2003 (2003-08), pages 396-405, XP008025253 the whole document in particular table 2 ----- -/--	1-27

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/012464

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2001 (2001-11-16), SCHOCH CLAUDIA ET AL: "Specific abnormalities on the genomic level result in a distinct gene expression pattern detected by oligonucleotide microarrays: An analysis of 25 patients with AML M2/t(8;21), AML M3/M3v/t(15;17), and AML M4eo/inv(16)" XP002269491 Database accession no. PREV200200129822 abstract & BLOOD, vol. 98, no. 11 Part 1, 16 November 2001 (2001-11-16), pages 92a-93a, 43rd Annual Meeting of the American Society of Hematology, Part 1;Orlando, Florida, USA; December 07-11, 2001 ISSN: 0006-4971	1-27
Y	EP 1 043 676 A (WHITEHEAD BIOMEDICAL INST) 11 October 2000 (2000-10-11) the whole document	1-27
Y	GOLUB T R ET AL: "Molecular classification of cancer: Class discovery and class prediction by gene expression monitoring" SCIENCE, AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE,, US, vol. 286, no. 5439, 15 October 1999 (1999-10-15), pages 531-537, XP002207658 ISSN: 0036-8075 cited in the application the whole document	1-27
Y	DUGAS M ET AL: "A comprehensive leukemia database: integration of cytogenetics, molecular genetics and microarray data with clinical information, cytomorphology and immunophenotyping" LEUKEMIA, MACMILLAN PRESS LTD, US, vol. 15, no. 12, December 2001 (2001-12), pages 1805-1810, XP002263731 ISSN: 0887-6924 the whole document	1-27

-/--

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DUGAS MARTIN ET AL: "Impact of integrating clinical and genetic information." IN SILICO BIOLOGY, vol. 2, no. 3, 2002, pages 383-391, XP001179418 ISSN: 1386-6338 (ISSN print) the whole document	1-27
A	CONNER SEAN D ET AL: "Identification of an adaptor-associated kinase, AAK1, as a regulator of clathrin-mediated endocytosis" JOURNAL OF CELL BIOLOGY, vol. 156, no. 5, 4 March 2002 (2002-03-04), pages 921-929, XP002270210 ISSN: 0021-9525 the whole document	1-27
A	ALIZADEH A ET AL: "THE LYMPHOCHIP: A SPECIALIZED CDNA MICROARRAY FOR THE GENOMIC-SCALE ANALYSIS OF GENE EXPRESSION IN NORMAL AND MALIGNANT LYMPHOCYTES" COLD SPRING HARBOR SYMPOSIA ON QUANTITATIVE BIOLOGY, BIOLOGICAL LABORATORY, COLD SPRING HARBOR, NY, US, vol. 64, no. 1, 1999, pages 71-78, XP001099007 ISSN: 0091-7451 the whole document	1-27
A	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), KOHLMANN ALEXANDER ET AL: "A Simplified and Partially Automated Target Preparation Method for Gene Expression Profiling." XP002269495 Database accession no. PREV200300367771 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 4287, 44th Annual Meeting of the American Society of Hematology;Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971	1-27

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2004/012464

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Article 52 (2)(d) EPC - Presentation of information

The claims were only searched with regards to the underlying method of generating a reference data base for distinguishing leukemia subtypes.

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-27 (partially)

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-27 (partially)

A method for distinguishing MLL-PTD-positive AML from other AML subtypes, the method comprising determining the expression level of the marker AAK1. Use of said marker for the manufacture of a diagnostic. A diagnostic kit containing said marker and an apparatus comprising a reference data bank, wherein the reference data bank is obtainable by determining the expression level of AAK1.

---

2. claims: 1-27 (all partially)

Inventions 2-1100

Methods for distinguishing MLL-PTD-positive AML from other AML subtypes and methods for distinguishing specific subtypes against all other subtypes and against each other, the method comprising determining individually the expression level of the markers listed in table 1.1, positions 2-50,and in tables 2-3. Use of said markers for the manufacture of diagnostics. Diagnostic kits containing said markers and apparatus comprising a reference data bank, wherein the reference data bank is obtainable by determining the expression levels of said markers.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/EP2004/012464

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 03039443 A	15-05-2003	EP 1308522 A1	07-05-2003
		WO 03039443 A2	15-05-2003
		EP 1470247 A2	27-10-2004
EP 1043676 A	11-10-2000	CA 2304876 A1	09-10-2000
		EP 1043676 A2	11-10-2000
		JP 2001017171 A	23-01-2001
		US 2003017481 A1	23-01-2003
		US 6647341 B1	11-11-2003
		US 2003073083 A1	17-04-2003

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

CORRECTED VERSION

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
12 May 2005 (12.05.2005)

PCT

(10) International Publication Number
WO 2005/043162 A2

(51) International Patent Classification[7]: G01N 33/574, C12Q 1/68

(21) International Application Number:
PCT/EP2004/012464

(22) International Filing Date:
4 November 2004 (04.11.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
03025339.7 4 November 2003 (04.11.2003) EP

(71) Applicant *(for DE only)*: **ROCHE DIAGNOSTICS GMBH** [DE/DE]; Sandhofer Str. 116, 68305 Mannheim (DE).

(71) Applicant *(for all designated States except DE, US)*: **F.HOFFMANN-LA ROCHE AG** [CH/CH]; Grenzacherstrasse 124, CH-4070 Basel (CH).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **HAFERLACH, Torsten** [DE/DE]; Springerstrasse 8, 81477 München (DE). **DUGAS, Martin** [DE/DE]; Michael-Fischer-Platz 6, 94469 Deggendorf (DE). **KERN, Wolfgang** [DE/DE]; Hanfelder Strasse 101, 82319 Starnberg (DE). **KOHLMANN, Alexander** [DE/DE]; Schwarzstrasse 14, 92318 Neumarkt (DE). **SCHNITTGER, Susanne** [DE/DE]; Saalburgstrasse 2a, 81375 München (DE). **SCHOCH, Claudia** [DE/DE]; Springerstrasse 8, 81477 München (DE).

(74) Common Representative: **ROCHE DIAGNOSTICS GMBH**; C/O Burger Alexander, Patent Department (TR-E), Postfach 11 52, 82372 Penzberg (DE).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

(48) Date of publication of this corrected version:
7 July 2005

(15) Information about Correction:
see PCT Gazette No. 27/2005 of 7 July 2005, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHOD FOR DISTINGUISHING MLL-PTD-POSITIVE AML FROM OTHER AML SUBTYPES

(57) Abstract: Disclosed is a method for distinguishing MLL-PTD-positive AML from other AML subtypes in a sample by determining the expression level of markers, as well as a diagnostic kit and an apparatus containing the markers.

WO 2005/043162 A2